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OW protein - protein search, using SW model

Run on: December 8, 2004, 08:30:16 ; Search time 187 Seconds
(without alignments)
15.384 Million cell updates/sec

Title: SEQ1
Perfect score: 26
Sequence: 1 devrp 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues
Total number of hits satisfying chosen parameters: 47

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-------------|---------------------|
| 1 | 11 | 42.3 | 4 | YIM1_YEAST | P36515 saccharomyc |
| 2 | 11 | 42.3 | 5 | TRM3_ECOLI | P13973 escherichia |
| 3 | 9 | 34.6 | 5 | UC22_MAIZE | P80628 zea mays 1m |
| 4 | 8 | 30.8 | 5 | BIOA_CITR | P13071 citrobacter |
| 5 | 8 | 30.8 | 5 | EIO3_LITRU | P82099 litorea rub |
| 6 | 8 | 30.8 | 5 | PARP_CHICK | P83308 gallus gall |
| 7 | 8 | 30.8 | 5 | PRCT_PERRAM | P01131 sus scrofa |
| 8 | 7 | 26.9 | 4 | THYL_PIG | P01373 periplaneta |
| 9 | 7 | 26.9 | 3 | DCML_PSRCH | P19916 pseudomonas |
| 10 | 7 | 26.9 | 4 | TUPT_HUMAN | P01858 homo sapien |
| 11 | 7 | 26.9 | 4 | Q16047 | P16047 homo sapien |
| 12 | 7 | 26.9 | 5 | BBP7_BOTIN | P30425 boctrops in |
| 13 | 7 | 26.9 | 5 | PAP2_PARMA | P81864 pardachirus |
| 14 | 7 | 26.9 | 5 | SUGA_ACHDO | P19991 acheta dome |
| 15 | 6 | 23.1 | 3 | LUXE_VIRBI | P24272 vibrio fisc |
| 16 | 6 | 23.1 | 4 | ACH1_ACHFU | P35904 achatina fu |
| 17 | 6 | 23.1 | 4 | OCPI_OCTMI | P58648 octopus min |
| 18 | 6 | 23.1 | 4 | OCPI_OCTMI | P58648 octopus min |
| 19 | 6 | 23.1 | 5 | MPA4_JUNVI | P81826 juniperus v |
| 20 | 6 | 23.1 | 5 | REI1_LITRU | P82070 litorea rub |
| 21 | 6 | 23.1 | 5 | UXA4_CHLTR | P38005 chlamydia t |
| 22 | 6 | 23.1 | 5 | P83073 | P83073 bacillus ce |
| 23 | 5 | 19.2 | 4 | EOSI_HUMAN | P07721 homo sapien |
| 24 | 5 | 19.2 | 4 | TIME_SEPOF | P83568 sepiia offic |
| 25 | 5 | 19.2 | 4 | Q08433 | Q08433 ratelus sp. |
| 26 | 5 | 19.2 | 5 | RE21_LITRU | P82071 litorea rub |
| 27 | 5 | 19.2 | 5 | RE31_LITRU | P82072 litorea rub |
| 28 | 4 | 15.4 | 5 | EIO4_LITRU | P82100 litorea rub |
| 29 | 4 | 15.4 | 5 | RE32_LITRU | P82073 litorea rub |
| 30 | 4 | 15.4 | 5 | TPIS_CANFA | P58714 canis famli |
| 31 | 3 | 11.5 | 4 | FYRI_ANTEU | P58706 antiopeura |

| | | | | | | |
|----|---|------|---|---|------------|---------------------|
| 32 | 3 | 11.5 | 5 | 1 | FARP_ARTTR | P41853 artiopeoschi |
| 33 | 3 | 11.5 | 5 | 1 | PSK_DAUCA | P58261 daucus caro |
| 34 | 3 | 11.5 | 5 | 1 | UP01_MOUSE | P38639 mus musculu |
| 35 | 2 | 7.7 | 5 | 2 | Q99007 | Q99007 hordium vul |
| 36 | 1 | 3.8 | 3 | 1 | GRWM_HUMAN | P01157 homo sapien |
| 37 | 1 | 3.8 | 4 | 1 | DCMS_PSECH | P42562 hirudo medi |
| 38 | 1 | 3.8 | 4 | 1 | FAR3_HIRME | P42563 hirudo medi |
| 39 | 1 | 3.8 | 4 | 1 | FAR4_HIRME | P58705 anthopleura |
| 40 | 1 | 3.8 | 4 | 1 | FRKA_ANTEU | P42561 hirudo medi |
| 41 | 1 | 3.8 | 4 | 1 | FLRN_HIRME | P58707 anthopleura |
| 42 | 1 | 3.8 | 4 | 1 | FLRN_ANTEU | P01162 macrocallis |
| 43 | 1 | 3.8 | 4 | 1 | FWRF_MACNI | Q9640 homo sapien |
| 44 | 1 | 3.8 | 4 | 2 | Q9640 | Q9640 homo sapien |
| 45 | 1 | 3.8 | 5 | 1 | AL14_CARMA | P81817 carcinus ma |

ALIGNMENTS

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RESULT 1
ID YIM1_YEAST STANDARD; PRT; 4 AA.
AC P36515;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Mitochondrial 60S ribosomal protein L1 (YIM1) (Fragment).
GN Name=YIM1;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE.
RX MEDLINE=91285106; PubMed=2060626;
RA Grohmann L., Graack H.-R., Kruff V., Choi T., Goldschmidt-Reisin S.,
RA Kitakawa M.,
RT "Extended N-terminal sequencing of proteins of the large ribosomal
RT subunit from yeast mitochondria."
RL FEBS Lett. 284:51-56(1991).
CC -!- FUNCTION: Putative component of the large subunit of mitochondrial
CC ribosome.
CC -!- SUBCELLULAR LOCATION: Mitochondrial.
CC
DR PIR; S17255; S17255.
KW Direct protein sequencing; Mitochondrion; Ribosomal protein.
FT NON TER 4
SQ SEQUENCE 4 AA; 402 MW; 7771B2D5D0000000 CRC64;

Query Match 42.3%; Score 11; DB 1; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVP 5
Db 2 VTP 4

RESULT 2
ID TRM3_ECOLI STANDARD; PRT; 5 AA.
AC P13973;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tram protein (Fragment).
GN Name=TRM3;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=88227859; PubMed=2836369;
RA Itanoto S., Yoshida Y., Ohtsubo E.;
RT "Identification and characterization of the products from the tral and
RT tral genes of plasmid R100."
RL J. Bacteriol. 170:2749-2757(1988).
CC -1- FUNCTION: Transfer gene protein. Is involved in the conjugation
CC process of bacterial cells for the exchange of plasmid DNA.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the tral family.
CC -----
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CC -----
DR EMBL; M20941; -; NOT_ANNOTATED_CDS.
DR PIR; A32014; A32014.
KM Conjugation; DNA-binding; Plasmid.
FT NON_TER
SQ SEQUENCE 5 AA; 634 MW; 6B1B1AA43500000 CRC64;

Query Match
Best Local Similarity 42.3%; Score 11; DB 1; Length 5;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DE 2
Db 3 DE 4

RESULT 3
UC22_MAIZE STANDARD; PRT; 5 AA.
ID UC22_MAIZE
AC P80628;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Unknown protein from 2D-PAGE of etiolated coleoptile (Spot 474)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP TISSUE=
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerwal C., Huot J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program."
RT Theor. Appl. Genet. 93:997-1005(1996).
CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 6.1, its MW is: 30.4 kDa.
CC Maize-2DPAGE; P80628; COLEOPTILE.
DR MaizeDB; 123954; -
KM Direct protein sequencing.
FT NON_TER
SQ SEQUENCE 5 AA; 654 MW; 72CB19C9C0300000 CRC64;

Query Match
Best Local Similarity 34.6%; Score 9; DB 1; Length 5;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EV 3
Db 4 EV 5

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RESULT 4
BIOA_CITFR STANDARD; PRT; 5 AA.
ID BIOA_CITFR
AC P13071;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Adenosylmethionine-8-amino-7-oxononanoate aminotransferase
DE (EC 2.6.1.62) (7,8-diamino-pelargonic acid aminotransferase) (DAPA
DE aminotransferase) (Fragment).
GN Name=BIOA;
OS Citrobacter freundii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Citrobacter.
OX NCBI_TaxID=546;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8906280; PubMed=2971595;
RA Shuan D., Campbell A.;
RT "Transcriptional regulation and gene arrangement of Escherichia coli,
RT Citrobacter freundii and Salmonella typhimurium biotin operons."
RL Gene 67:203-211(1988).
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 8-amino-7-
CC oxononanoate = S-adenosyl-4-methylthio-2-oxobutanoate + 7,8-
CC diaminononanoate.
CC -1- COFACTOR: Pyridoxal phosphate.
CC -1- PATHWAY: Biotin biosynthesis.
CC -1- SUBUNIT: Homodimer.
CC -1- SIMILARITY: Belongs to the class-III pyridoxal-phosphate-dependent
CC aminotransferase family.
CC -----
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CC -----
DR EMBL; M21922; -; NOT_ANNOTATED_CDS.
DR PIR; I40697; I40697.
DR InterPro; IPR005814; Aminotrans_3.
DR PROSITE; PS00600; AA TRANSFER CLASS 3; PARTIAL.
KM Aminotransferase; Biotin biosynthesis; Pyridoxal phosphate;
KM Transferase.
FT NON_TER
SQ SEQUENCE 5 AA; 582 MW; 6AAAB1B1A6F00000 CRC64;

Query Match
Best Local Similarity 30.8%; Score 8; DB 1; Length 5;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DE 2
Db 4 DD 5

RESULT 5
BIO3_LITRU STANDARD; PRT; 5 AA.
ID BIO3_LITRU
AC P82099;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Electrin 3.
OS Iltoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
OC Pelodyadinae; Iltoria.
OX NCBI_TaxID=104695;
RN [1]
RP TISSUE=
RC TISSUE=Skin secretion;

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RA Mabiniz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella."
RL Aust. J. Chem. 52:639-645(1999).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
KW Amidation; Amphibian defense peptide; Direct protein sequencing.
FT MOD_RES 5
SQ SEQUENCE 5 AA; 630 MW; 668761F2C9A00000 CRC64;

Query Match 30.8%; Score 8; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. NO. 1.8e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVP 5
DB 2 VHP 4

RESULT 6
FARP CHICK STANDARD; PRT; 5 AA.
AC P83308;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE FMRamide-like neuropeptide (LPLRF-amide).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RN SEQUENCE, AND SYNTHESES.
RC TISSUE=Brain;
RX PubMed=6137771;
RT Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;
RT "A novel active pentapeptide from chicken brain identified by
RT antibodies to FMRamide."
RL Nature 305:328-330(1983).
CC -1- FUNCTION: May function as a neurotransmitter or modulator.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
CC family.
DR GO:0007218; P:neuropeptide signaling pathway; TMS.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 5
SQ SEQUENCE 5 AA; 645 MW; 69D4073767400000 CRC64;

Query Match 30.8%; Score 8; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. NO. 1.8e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 VP 5
DB 1 LP 2

RESULT 7
PRCT PERAM STANDARD; PRT; 5 AA.
ID P01373;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Proctolin.
OS Periplaneta americana (American cockroach),
OS Limulus polyphemus (Atlantic horseshoe crab), and
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattelloidea;
OC Blattidae; Periplaneta.

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OX NCBI_TaxID=6978, 6850, 6759;
RN [1]
RN SEQUENCE.
RP SPECIES=P.americana;
RX MEDLINE=76074708; PubMed=576;
RA Starrett A.N., Brown B.E.;
RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter
RT in insects."
RL Life Sci. 17:1253-1256(1975).
RN [2]
RN BIOLOGICAL SOURCE.
RP SPECIES=P.americana;
RX MEDLINE=81225865; PubMed=6113690;
RA O'Shea M., Adams M.E.;
RT "Pentapeptide (proctolin) associated with an identified neuron."
RL Science 213:567-569(1981).
RN [3]
RN SEQUENCE.
RP SPECIES=L.polyphemus;
RX MEDLINE=90287800; PubMed=2356151;
RA Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,
RA Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
RA Shabanowitz J.;
RT "Identification of proctolin in the central nervous system of the
RT horseshoe crab, Limulus polyphemus."
RL Peptides 11:205-211(1990).
RN [4]
RN SEQUENCE.
RP SPECIES=C.maenas;
RX MEDLINE=86232789; PubMed=2872661;
RA Stangier J., Dirksen H., Keller R.;
RT "Identification and immunocytochemical localization of proctolin in
RT pericardial organs of the shore crab, Carcinus maenas."
RL Peptides 7:67-72(1986).
CC -1- FUNCTION: Stimulates cardiac output and hindgut motility,
CC modulates visceral and skeletal muscle in many arthropods.
CC -1- TISSUE SPECIFICITY: Found in the lateral white neurons and in the
CC crab pericardial organs.
DR PIR: A01644; HOROHA.
DR PIR: A60411; A60411.
KW Direct protein sequencing; Neuropeptide.
SQ SEQUENCE 5 AA; 649 MW; 71B7673B44600000 CRC64;

Query Match 30.8%; Score 8; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. NO. 1.8e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 VP 5
DB 3 LP 4

RESULT 8
THYL_PIG STANDARD; PRT; 3 AA.
ID P01151;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Thyroliberin (Thyrotropin releasing hormone) (TRH) (Proctirelin).
OS Sus scrofa (Pig).
OS Ovis aries (sheep),
OS Bombina orientalis (Oriental fire-bellied toad), and
OS Notoptalmus viridescens (Eastern newt) (Triturus viridescens).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
CX NCBI_TaxID=9823, 9940, 8346, 8316;
RN [1]
RN SEQUENCE.
RP SPECIES=Pig; TISSUE=Hypothalamus;
RX MEDLINE=70136150; PubMed=4984938;
RA Nair R.M.G., Barrett J.F., Bowers C.Y., Schally A.V.;
RT "Structure of porcine thyrotropin releasing hormone."

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RL Biochemistry 9:1103-1106(1970).
 RN [2]
 RP SYNTHESIS.
 RC SPECIES=Plg;
 RX MEDLINE=70039904; PubMed=4982117;
 RA Boler J., Enzmann F., Folkers K., Bowers C.V., Schally A.V.;
 RT "The identity of chemical and hormonal properties of the thyrotropin
 releasing hormone and pyroglutamyl-histidyl-proline amide.";
 RL Biochem. Biophys. Res. Commun. 37:705-710(1969).
 RN [3]
 RP SEQUENCE.
 RC SPECIES=Sheep; TISSUE=Hypothalamus;
 RA Desiderio D.M. Jr., Burgess R., Dunn T.F., Vale W., Guillemin R.,
 RA Ward D.N.;
 RT "The elucidation of the primary structure of the hypothalamic thyroid
 stimulating hormone releasing factor of ovine origin by means of mass
 spectrometry.";
 RL Org. Mass Spectrom. 5:221-228(1971).
 RN [4]
 RP SYNTHESIS.
 RC SPECIES=Sheep;
 RX MEDLINE=70163386; PubMed=4985794;
 RA Burgess R., Dunn T.F., Desiderio D.M., Ward D.N., Vale W.,
 RA Guillemin R.;
 RT "Characterization of ovine hypothalamic hypophysiotropic TSH-releasing
 factor.";
 RL Nature 226:321-325(1970).
 RN [5]
 RP SEQUENCE.
 RC SPECIES=B.orientalis; TISSUE=Skin;
 RX MEDLINE=76138399; PubMed=815011;
 RA Yasuhara T., Nakajima T.;
 RT "Occurrence of Pyr-His-Pro-NH2 in the frog skin.";
 RL Chem. Pharm. Bull. 23:3301-3303(1975).
 RN [6]
 RP SEQUENCE.
 RC SPECIES=N.viridescens;
 RX MEDLINE=75035605; PubMed=4214528;
 RA Grimm-Joergensen Y., McKelvy J.F.;
 RT "Biosynthesis of thyrotropin releasing factor by new (Triturus
 viridescens) brain in vitro. Isolation and characterization of
 thyrotropin releasing factor.";
 RL J. Neurochem. 23:471-478(1974).
 CC -1- FUNCTION. TSH functions as a regulator of the biosynthesis of TSH
 in the anterior pituitary gland and as a neurotransmitter/
 neuromodulator in the central and peripheral nervous systems.
 CC PIR; A90919; RHTDTC.
 DR PIR; A92971; A92971.
 DR PIR; A93750; RHSH.
 KM Annotation: Direct protein sequencing; Pyrolytic carboxylic acid.
 FT MOD_RES 1 1 Pyrolytic carboxylic acid.
 FT MOD_RES 3 3 Proline amide.
 SQ SEQUENCE 3 AA; 380 MW; 7761F6B000000000 CRC64;
 Query Match 26.9%; Score 7; DB 1; Length 3;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 P 5
 DB 3 P 3
 ID DCML_PSECH STANDARD; PRT; 4 AA.
 AC P19916;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (CO
 dehydrogenase subunit L) (CO-DH L) (Fragment).
 GN Name=culL;

OS Pseudomonas carboxydohydrogena.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae.
 OX NCBI_TaxID=290;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90055678; PubMed=2818128;
 RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
 RT "Homology and distribution of CO dehydrogenase structural genes in
 carboxydophilic bacteria.";
 RL Arch. Microbiol. 152:335-341(1989).
 CC -1- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
 dioxide.
 CC -1- CATALYTIC ACTIVITY: CO + H(2)O + A = CO(2) + AH(2).
 CC -1- COPACOR: Binds 1 copper(I) ion, 1 molybdenum(VI) ion and 1
 molybdopterin cytosine dinucleotide (MCD) per subunit.
 CC -1- SUBUNIT: Heterotrimer consisting of a large, a medium and a small
 subunit.
 DR PIR; PL0140; PL0140.
 KM Direct protein sequencing; Molybdenum; Oxidoreductase.
 FT NON TER 4
 SQ SEQUENCE 4 AA; 441 MW; 7761E876F0000000 CRC64;
 Query Match 26.9%; Score 7; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 P 5
 DB 4 P 4
 ID TUFT_HUMAN STANDARD; PRT; 4 AA.
 AC P01858;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Phagocytosis-stimulating peptide (tuftsin).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 CC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=72187087; PubMed=4112769;
 RA Nishioka K., Constantopoulos A., Satoh P.S., Najjar V.A.;
 RT "The characteristics, isolation and synthesis of the phagocytosis
 stimulating peptide tuftsin.";
 RL Biochem. Biophys. Res. Commun. 47:172-179(1972).
 RN [2]
 RP IMMUNOGLOBULIN CLAS.
 RX MEDLINE=68091045; PubMed=4169272;
 RA Fidalgo B.V., Najjar V.A.;
 RT "The physiological role of the lymphoid system. VI. The stimulatory
 effect of leucophilic gamma globulin (leucokinin) on the phagocytic
 activity of human polymorphonuclear leucocyte.";
 RL Biochemistry 6:3386-3392(1967).
 CC -1- MISCELLANEOUS: An IgG (called leucokinin) binds reversibly to the
 cell membrane of neutrophils in the blood. Leucokininase on the
 membrane releases the active peptide tuftsin from the gamma chain.
 CC Tuftsin is essential for maximum stimulation of the phagocytic
 activity of neutrophils.
 DR PIR; A02147; A02147.
 DR MIM; 191150; .
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006909; P:phagocytosis; NAS.
 KM Direct protein sequencing. 74176321C000000000 CRC64;
 SQ SEQUENCE 4 AA; 501 MW; 74176321C000000000 CRC64;
 Query Match 26.9%; Score 7; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 P 5
1
3 P 3

Db

RESULT 11

Q16047 PRELIMINARY; PRT; 4 AA.

AC 016047;
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
DE Interleukin 2 receptor alpha-subunit (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxId=9606;
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92062171; PubMed=1840490;
RA Mercken L., Moras V., Hemon L., Lione B., Bousseau A.,
RA Dautry-Varat A., Collin M., Mayaux J.F.;
RT "An exon 5-deleted mRNA encodes a functional interleukin 2 receptor
alpha-subunit.";
RT Biochem. Biophys. Res. Commun. 180:1390-1395(1991).
RL EMBL; S64248; AAB20279.1; .
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001806; Ras_trnfrmg.
DR Pfam; PF00071; Ras; 1.
DR PRINTS; PRO0449; RASTRNSFRMG.
KM GTP-binding: Receptor.
FT NON_TER 4
SQ SEQUENCE 4 AA; 525 MW; 69CAB769A0000000 CRC64;

Query Match 26.9%; Score 7; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 P 5
1
2 P 2

Db

RESULT 12

BPP7_BOTIN STANDARD; PRT; 5 AA.

ID BPP7_BOTIN
AC P30425;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Bradykinin-potentiating peptide S5,2 (5A) (Angiotensin-converting
enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OC NCBI_TaxId=8723;
OX NCBI_TaxId=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=238615;
RA Cincira A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
DE -1- FUNCTION: This peptide both inhibits the activity of the
angiotensin-converting enzyme and enhances the action of
bradykinin by inhibiting the kinases that inactivate it. It acts
as an indirect hypotensive agent.

DR PIR; G37196; G37196.
KM Direct protein sequencing; Hypotensive agent;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1
SQ SEQUENCE 5 AA; 629 MW; 776DC37326B00000 CRC64;

Query Match 26.9%; Score 7; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 P 5
1
5 P 5

Db

RESULT 13

PAR2_PARMA STANDARD; PRT; 5 AA.

ID PAR2_PARMA
AC P81864;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pardaxin II (PXII) (Fragment).
OS Pardaxin marmoratus (Red sea moses sole).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Pleuronectiformes;
OC Soleiidae; Soleidae; Pardaxin.
OC NCBI_TaxId=31087;
OX NCBI_TaxId=31087;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=87057369; PubMed=3782138;
RA Lazarovici P., Primor N., Loew J.M.;
RT "Purification and pore-forming activity of two hydrophobic
polypeptides from the secretion of the Red sea moses sole (Pardaxin
marmoratus).";
RT J. Biol. Chem. 261:16704-16713(1986).
RL -1- FUNCTION: Exhibits unusual shark repellent and surfactant
properties. Forms voltage-dependent, ion-permeable channels in
membranes. At high concentration causes cell membrane lysis.
CC -1- SUBUNIT: Monomer. In aqueous solution exists as a tetramer.
CC -1- SUBUNIT: Monomer. In aqueous solution exists as a tetramer.
CC -1- SIMILARITY: Belongs to the pardaxin family.
KM Direct protein sequencing; Toxin.
FT NON_TER 5
SQ SEQUENCE 5 AA; 614 MW; 7769C9C9C8100000 CRC64;

Query Match 26.9%; Score 7; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 P 5
1
5 P 5

Db

RESULT 14

SUGA_ACHDO STANDARD; PRT; 5 AA.

ID SUGA_ACHDO
AC P19991;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Suboesophageal ganglion pentapeptide.
OS Acheta domestica (House cricket).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;
OC Acheta.
OC NCBI_TaxId=6997;
OX NCBI_TaxId=6997;
RN [1]
RP SEQUENCE.
RC WICKER C., WICKER C.;

RT "Isolation and structure of a peptide isolated from the subesophageal
 RT ganglion of Acheeta domesticus (Orthoptera).";
 RL Comp Biochem. Physiol. 88C:185-187(1987).
 CC -1- SUBCELLULAR LOCATION: Main peptide from the subesophageal
 CC ganglia.
 DR PIR: J50319; J50319.
 DR Direct protein sequencing.
 SQ SEQUENCE 5 AA; 476 MW; 69D76DDDD80000 CRC64;

Query Match 26.9%; Score 7; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 P 5
 DB 4 P 4

RESULT 15
 LUXE_VIBF1
 ID LUXE_VIBF1 STANDARD; PRT; 3 AA.
 AC P24272;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Long-chain-fatty-acid--luciferin-component ligase (EC 6.2.1.19) (Acyl-
 DE protein synthetase) (Fragment).
 GN Name=luxe;
 OS Vibrio fischeri.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 OX NCBI_TaxID=668;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91072226; PubMed=2254256;
 RA Swartzman E., Kapoor S., Graham A.F., Meighen E.A.;
 RT "A new Vibrio fischeri lux gene precedes a bidirectional termination
 RT site for the lux operon."
 RL J. Bacteriol. 172:6797-6802(1990).
 CC -1- FUNCTION: Acyl-protein synthetase activates tetradecanoic acid. It
 CC is a component of the fatty acid reductase complex responsible for
 CC converting tetradecanoic acid to the aldehyde which serves as
 CC substrate in the luciferase-catalyzed reaction.
 CC -1- CATALYTIC ACTIVITY: ATP + an acid + protein = AMP + diphosphate +
 CC an acyl-protein thioester.
 CC -1- PATHWAY: Bioluminescent fatty acid reduction system; second step.
 CC -1- SIMILARITY: Belongs to the luxe family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M62812; -; NOT_ANNOTATED_CDS.
 DR Ligase; Luminescence.
 KM NON_TER 1
 FT SEQUENCE 3 AA; 374 MW; 6AA3303000000000 CRC64;
 SQ

Query Match 23.1%; Score 6; DB 1; Length 3;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 D 1
 DB 3 D 3

Search completed: December 8, 2004, 08:51:54
 Job time : 190 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 08:31:09 ; Search time 159 Seconds
(Without alignments)
11.281 Million cell updates/sec

Title: SEQ1
Perfect score: 26
Sequence: 1 decomp 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 35872929 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 26 | 100.0 | 5 | 4 | AAB66374 |
| 2 | 26 | 100.0 | 5 | 5 | ABG31916 |
| 3 | 26 | 100.0 | 5 | 7 | ABU61522 |
| 4 | 26 | 100.0 | 5 | 7 | ABU61519 |
| 5 | 26 | 100.0 | 6 | 4 | AAM52534 |
| 6 | 26 | 100.0 | 6 | 4 | AAB67389 |
| 7 | 26 | 100.0 | 6 | 4 | AAB66359 |
| 8 | 26 | 100.0 | 6 | 4 | AAB66377 |
| 9 | 26 | 100.0 | 6 | 4 | AAB66384 |
| 10 | 26 | 100.0 | 6 | 4 | AAG64159 |
| 11 | 26 | 100.0 | 6 | 5 | ABG31912 |
| 12 | 26 | 100.0 | 6 | 5 | ABG31915 |
| 13 | 26 | 100.0 | 6 | 5 | ABR05374 |
| 14 | 26 | 100.0 | 6 | 5 | ABG32506 |
| 15 | 26 | 100.0 | 6 | 5 | ABG74004 |
| 16 | 26 | 100.0 | 9 | 6 | ABG74004 |
| 17 | 26 | 100.0 | 9 | 6 | ABG74004 |
| 18 | 26 | 100.0 | 58 | 1 | AAP81263 |
| 19 | 26 | 100.0 | 72 | 1 | AAP50049 |
| 20 | 26 | 100.0 | 74 | 1 | AAP50047 |
| 21 | 26 | 100.0 | 74 | 1 | AAP82689 |
| 22 | 26 | 100.0 | 75 | 1 | AAP71201 |
| 23 | 26 | 100.0 | 78 | 4 | AAB09778 |
| 24 | 26 | 100.0 | 96 | 4 | AAB45914 |
| 25 | 26 | 100.0 | 96 | 6 | ABM42433 |

| | | | | | |
|----|----|-------|-----|---|----------|
| 26 | 26 | 100.0 | 98 | 8 | ADP99245 |
| 27 | 26 | 100.0 | 100 | 6 | ABM71931 |
| 28 | 26 | 100.0 | 108 | 4 | AAU42592 |
| 29 | 26 | 100.0 | 108 | 6 | ABM39111 |
| 30 | 26 | 100.0 | 108 | 6 | ABM65718 |
| 31 | 26 | 100.0 | 120 | 4 | AAE02771 |
| 32 | 26 | 100.0 | 120 | 4 | AAU57682 |
| 33 | 26 | 100.0 | 120 | 6 | ABM54201 |
| 34 | 26 | 100.0 | 120 | 8 | ADQ30924 |
| 35 | 26 | 100.0 | 125 | 1 | AAP82656 |
| 36 | 26 | 100.0 | 125 | 8 | ADJ71222 |
| 37 | 26 | 100.0 | 126 | 1 | AAP50037 |
| 38 | 26 | 100.0 | 126 | 1 | AAP51240 |
| 39 | 26 | 100.0 | 126 | 2 | AAP00582 |
| 40 | 26 | 100.0 | 126 | 2 | AAW34533 |
| 41 | 26 | 100.0 | 128 | 8 | ADP99246 |
| 42 | 26 | 100.0 | 130 | 7 | ADD71229 |
| 43 | 26 | 100.0 | 130 | 7 | ADD71230 |
| 44 | 26 | 100.0 | 130 | 7 | ADD71231 |
| 45 | 26 | 100.0 | 130 | 8 | ADJ71224 |

ALIGNMENTS

RESULT 1
AAB66374 standard; peptide; 5 AA.
XX

AAB66374:

09-APR-2001 (first entry)
Hepatitis C virus protease inhibitor boronic acid peptide #20.

Hepatitis C virus; protease; boronic acid; inhibitor; liver cirrhosis;
KM liver cancer; NS3; antiviral agent.

XX
OS Synthetic.

XX
FH Key Location/Qualifiers

FT Modified-site 1 /label= OTHER

FT FT /note= "optionally Boc-Asp(OtBu) or Ac-Asp(OtBu)"

FT Modified-site 2 /label= OTHER

FT FT /note= "Glu(OtBu)"

XX
FM W0200102424-A2.

XX
PD 11-JAN-2001.

XX
PF 07-JUL-2000; 2000WO-US018655.

XX
PR 07-JUL-1999; 99US-0142561P.

XX
PA (DUPO) DU PONT PHARM CO.

XX
PI Ketchner CA, Jagannathan S, Forsyth TP;

XX
DR WPI, 2001-103001/11.

XX
PT New boronic acid derivatives, optionally containing peptides, used to

PT treat hepatitis C infections, are hepatitis C viral protease inhibitors.

XX
PS Example 9; Page 127; 258PP; English.

XX
CC The present invention provides a number of boronic acid derivatives which

CC act as inhibitors of the hepatitis C virus NS3 protease enzyme. They can

CC be used to treat infection by the virus, which can cause liver cirrhosis

XX
CC and liver cancer

XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 26; DB 4; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVVP 5
 DB 1 DEVVP 5

RESULT 2
 ABG31916

ID ABG31916 standard; peptide; 5 AA.

AC ABG31916;

DT 05-NOV-2002 (first entry)

DE HCV serine protease imidazolidinone inhibitor #2.

KW HCV; hepatitis C; imidazolidinone; serine protease inhibitor; virucide;
 KW heptotrophic; antiinflammatory; NS3 protease; growth inhibitor;
 KW viral infection; blood plasma processing.

OS Synthetic.

Key Location/Qualifiers
 Modified-site 1 /label= OTHER

FT Misc-difference 2 /note= "OTHER= Boc-Asp (OCBu) "

FT Modified-site 5 /note= "Glu(OCBu) "

FT /label= OTHER
 /note= "OTHER= Hydroxyl group"

PN W0200248157-A2.

PD 20-JUN-2002.

PF 12-DEC-2001; 2001WO-US047916.

PR 13-DEC-2000; 2000US-0255168P.

PA (BRIM) BRISTOL MYERS SQUIBB PHARMA CO.

PI Han Q;

WI; 2002-559498/64.

PT New imidazolidinones useful as serine protease inhibitors in the
 treatment of e.g. viral infection.

PS Example 20; Page 115; 173pp; English.

CC This invention relates to novel imidazolidinones or their stereoisomers,
 CC salts or produgs which are useful as serine protease inhibitors. The
 CC imidazolidinones of the invention may have virucide, hepatotropic, or
 CC antiinflammatory activities and may be used as a serine protease
 CC inhibitor (preferably Hepatitis C virus (HCV) NS3 protease inhibitor) or
 CC a HCV growth inhibitor. Compounds of the invention are useful for
 CC treating viral infection e.g. hepatitis C virus (HCV) infection and as a
 CC reagent used as inhibitors of HCV protease in the processing of blood
 CC plasma for diagnostic and other commercial purposes. The imidazolidinones
 CC of the invention inhibit HCV NS3 protease and/or HCV growth and thus can
 CC be used in the blood plasma assay. The present sequence represents a
 CC imazolidinone protease inhibitor shown in the examples of the
 CC specification

Sequence 5 AA;

Query Match 100.0%; Score 26; DB 5; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVVP 5
 DB 1 DEVVP 5

RESULT 3
 ABU61522

ID ABU61522 standard; peptide; 5 AA.

AC ABU61522;

DT 08-AUG-2003 (first entry)

DE Hepatitis C virus NS3 protease inhibitor peptide.

KW Hepatitis C virus; NS3 protease; hepatotropic; virucide;
 KW antiinflammatory; serine protease inhibitor; hepatitis C virus;
 KW NS3 Protease inhibitor; viral infection; elastase; chymotrypsin.

OS Synthetic.

Key Location/Qualifiers
 Modified-site 1 /label= O-CBu (not defined)

FT Modified-site 1 /note= "Boc (not defined) "

FT Modified-site 2 /note= "O-CBu (not defined) "

FT Modified-site 5 /note= "C-terminal hydroxyl"

PN US2002177725-A1.

PD 28-NOV-2002.

PF 28-OCT-2001; 2001US-00039317.

PR 23-OCT-2000; 2000US-0242557P.

PA (PRIE/) PRIESTLEY E S.

PI Priestley ES;

WI; 2003-465950/44.

PT New class of peptides are inhibitors of hepatitis C virus NS3 protein,
 useful for treating e.g. hepatitis.

PS Example 1; Page 27; 54pp; English.

CC The invention describes novel peptide useful for treating viral
 CC infections e.g. Hepatitis C virus (HCV) infections. The compounds have
 CC HCV NS3 protease inhibitory selectivity over inhibition of elastase and
 CC chymotrypsin. This is the amino acid sequence of a modified peptide
 CC associated with an assay of NS3 protease activity

Sequence 5 AA;

Query Match 100.0%; Score 26; DB 7; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVVP 5
 DB 1 DEVVP 5

RESULT 4

ABU61519
 ID ABU61519 standard; peptide; 5 AA.

AC AB061519;
 XX 08-AUG-2003 (first entry)
 DT
 XX Hepatitis C virus NS3 protease inhibitor.
 DE
 XX Hepatitis C virus; NS3 protease; hepatotropic; virucide;
 KM antiinflammatory; serine protease inhibitor; hepatitis C virus;
 KM NS3 protease inhibitor; viral infection; elastase; chymotrypsin.
 XX
 OS Synthetic.
 XX
 FH Key
 FT Modified-site
 FT 5 Location/Qualifiers
 FT /note= "(1R)-1-amino-3-phenylpropylboronic acid (+)-
 FT pinanediol ester, or (1R)-1-amino-4-phenylbutylboronic
 FT acid (+)-pinanediol ester, (1R)-amino-5-
 FT phenylbutylboronic acid (+)-pinanediol ester, or (1R)-1-
 FT amino-3-(2-naphthyl)propylboronic acid (+)-pinanediol
 FT ester, or (1R)-1-amino-3-(2-methylphenyl)propylboronic
 FT acid (+)-pinanediol ester, or (1R)-1-amino-3-(3-
 FT methylphenyl)propylboronic acid (+)-pinanediol ester, or
 FT (1R)-1-amino-3-(4-methylphenyl)propylboronic acid (+)-
 FT pinanediol ester, or (1R)-1-amino-3-(1,1'-biphenyl)-4-
 FT ylpropylboronic acid (+)-pinanediol ester, or (1R)-1-
 FT amino-3-(2,5-dimethylphenyl)propylboronic acid (+)-
 FT pinanediol ester, or (1R)-1-amino-3-(2,4-
 FT dimethylphenyl)propylboronic acid (+)-pinanediol ester, or
 FT (1R)-1-amino-3-(4-trifluoromethylphenyl)propylboronic
 FT acid (+)-pinanediol ester, or (1R)-1-amino-3-(3-
 FT trifluoromethylphenyl)propylboronic acid (+)-pinanediol
 FT ester, or (1R)-1-amino-3-(4-fluoro)phenylpropylboronic
 FT acid (+)-pinanediol ester, or (1R)-1-amino-3-
 FT (40phenoxylphenyl)propylboronic acid (+)-pinanediol ester,
 FT or (1R)-1-amino-3-(4-isopropylphenyl)propylboronic acid
 FT (+)-pinanediol ester, or (1R)-1-amino-3-(4-cyclohexyl)
 FT phenylpropylboronic acid (+)-pinanediol ester, or (1R)-1-
 FT amino-3-(4-tert-butylphenyl)propylboronic acid (+)-
 FT pinanediol ester, or (1R)-1-amino-3-(4-
 FT methoxyphenyl)propylboronic acid (+)-pinanediol ester, or
 FT methoxyphenylpropylboronic acid (+)-pinanediol ester, or
 FT (1R)-1-amino-3-(4-chlorophenyl)propylboronic acid (+)-
 FT pinanediol ester, or (1R)-1-amino-3-(4-bromo)
 FT phenylpropylboronic acid (+)-pinanediol ester, or (1R)-1-
 FT amino-3-(2-fluoro)phenylpropylboronic acid (+)-pinanediol
 FT ester, or (1R)-1-amino-3-(3-fluoro)phenylpropylboronic
 FT acid (+)-pinanediol ester, or (1R)-1-amino-3-(2,6-
 FT difluoro)phenylpropylboronic acid (+)-pinanediol ester,
 FT or (1R)-1-amino-3-(4-hydroxyphenyl)propylboronic acid (+)-
 FT pinanediol ester, or (1R)-1-amino-5-methylhexylboronic
 FT acid (+)-pinanediol ester, or (1R)-1-amino-4-
 FT cyclobutylbutylboronic acid (+)-pinanediol ester, or (1R)
 FT -1-amino-5-ethylheptylboronic acid (+)-pinanediol ester.
 FT 1R is not defined."
 FT
 XX
 XX US2002177725-A1.
 XX
 XX 28-NOV-2002.
 XX
 XX 28-OCT-2001; 2001US-00039317.
 XX
 XX 23-OCT-2000; 2000US-0242557P.
 XX
 XX (PRIE/) PRIESTLEY E S.
 XX
 XX Priestley ES;
 XX
 XX WPI; 2003-465950/44.
 XX
 XX
 XX New class of peptides are inhibitors of hepatitis C virus NS3 protein,
 XX useful for treating e.g. hepatitis.

PS Example; Page 14-15; 54pp; English.
 XX
 XX The invention describes novel peptide useful for treating viral
 CC infections e.g. Hepatitis C virus (HCV) infections. The compounds have
 CC HCV NS3 protease inhibitory selectivity over inhibition of elastase and
 CC chymotrypsin. This is the amino acid sequence of a modified peptide that
 CC functions as an NS3 inhibitor
 XX
 XX Sequence 5 AA;
 SQ
 Query Match 100.0%; Score 26; DB 7; Length 5;
 Best local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DEVP 5
 DB 1 DEVP 5
 RESULT 5
 ID AAM52534
 AAM52534 standard; peptide; 6 AA.
 XX
 XX AAM52534;
 DT 31-JAN-2002 (first entry)
 XX
 XX NS3 protease peptide inhibitor #1.
 DE
 XX
 XX virucide; pyrolopyrazinone derivative; Hepatitis C virus inhibitor;
 KM nonstructural 3 protease; NS3 protease; viral infection.
 XX
 XX Synthetic.
 OS
 FH Key
 FT Modified-site
 FT 1 Location/Qualifiers
 FT /note= "Optionally Boc-Asp (OtBu) or H-Asp"
 FT Modified-site
 FT 2 /note= "Optionally Glu(OtBu) or Glu"
 FT Modified-site
 FT 5 /note= "Optionally Pro-boroAlg-OH, Pro-OH or Pro-boroAlg-
 FT pinanediol, where Alg is 2-amino-4-pentenoic acid"
 FT
 XX
 XX WO200164678-A2.
 XX
 XX 07-SEP-2001.
 XX
 XX 28-FEB-2001; 2001WO-US006269.
 XX
 XX 29-FEB-2000; 2000US-0185618P.
 XX
 XX (DUPO) DUPONT PHARM CO.
 XX
 XX Zhang X, Han W;
 XX
 XX WPI; 2001-656752/75.
 XX
 XX New pyrolopyrazinone derivatives useful for treating Hepatitis C virus
 XX infection are NS3 protease inhibitors.
 XX
 XX Disclosure; Page 130; 191pp; English.
 XX
 XX The present invention relates to a novel pyrolopyrazinone derivative,
 CC its stereoisomer or salt. It was found that the derivative is a Hepatitis
 CC C virus (HCV) nonstructural (NS) 3 protease inhibitor. The derivative is
 CC useful for the manufacture of a medicament for the treatment of HCV and
 CC in therapy for treating HCV infection. The present peptide is a peptide
 CC inhibitor for HCV NS3 protease, which was used to illustrate the present
 CC invention
 XX
 XX Sequence 6 AA;
 SQ
 Query Match 100.0%; Score 26; DB 4; Length 6;

Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVVP 5
Db 1 DEVVP 5

RESULT 6
AAB67389

ID AAB67389 standard; peptide; 6 AA.

AC AAB67389;

DT 26-APR-2001 (first entry)

DE Protease inhibitor.

KW Lactam; hepatitis C virus; HCV; NS3 protease.

OS Synthetic.

PN WO200107407-A1.

PD 01-FEB-2001.

PF 26-JUL-2000; 2000WO-US020189.

PR 26-JUL-1999; 99US-0145631P.

PA (DUPO) DU PONT PHARM CO.

PI Priestley ES, Decicco CP;

DR WPI; 2001-159696/16.

PT New lactam derivatives are hepatitis C virus NS3 protease inhibitors
useful for treating HCV infections.

PS Example 26; Page 100; 130pp; English.

CC The present invention relates to lactam derivatives. These derivatives
may be used for treating hepatitis C virus (HCV) infection. They can also
be used for inhibiting HCV in a body fluid sample and as a standard or
reagent in a test or assay for determining the ability of a potential
pharmaceutical to inhibit HCV NS3 protease and/or HCV growth

XX Sequence 6 AA;

Query Match 100.0%; Score 26; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVVP 5
Db 1 DEVVP 5

RESULT 7
AAB66359

ID AAB66359 standard; peptide; 6 AA.

AC AAB66359;

DT 09-APR-2001 (first entry)

DE Hepatitis C virus protease inhibitor boronic acid peptide #9.

KW Hepatitis C virus; protease; boronic acid; inhibitor; liver cirrhosis;

KW liver cancer; NS3; antiviral agent.

OS Synthetic.

XX

FH Key Location/Qualifiers
FT Modified-site 1

FT /label= OTHER

FT /note= "optionally Boc-Asp(OTBu), Ac-Asp(OTBu) or Ac-Asp"

FT /label= OTHER

FT /note= "optionally Glu(OTBu), optionally D-form residue"

FT /label= OTHER

FT /note= "optionally boro-L-2-amino-3-cyclopropylpropionic
(borocPa) acid pinanediol ester. borocPa pinanediol,
borocPa pinanediol ester.Hcl, boro-L-2-amino-4-pentenoic
acid (boroa1g) pinanediol, boroa1g pinanediol
ester.trifluoroacetate, boroa1g-ClOH16, boroa1g, boroape-
pinanediol, boroape-pinanediol.Hcl, boro-L-4',4'-difluoro-
1-amino-butyric acid (borodFb) pinanediol or borodFb
pinanediol ester.hydrochloride"

PN WO200102424-A2.

PD 11-JAN-2001.

PF 07-JUL-2000; 2000WO-US018655.

PR 07-JUL-1999; 99US-0142561P.

PA (DUPO) DU PONT PHARM CO.

PI Kettner CA, Jagannathan S, Forsyth TP;

DR WPI; 2001-103001/11.

PT New boronic acid derivatives, optionally containing peptides, used to
treat hepatitis C infections, are hepatitis C viral protease inhibitors.

PS Example 7; Page 255; 258pp; English.

CC The present invention provides a number of boronic acid derivatives which
act as inhibitors of the hepatitis C virus NS3 protease enzyme. They can
be used to treat infection by the virus, which can cause liver cirrhosis
and liver cancer

XX Sequence 6 AA;

Query Match 100.0%; Score 26; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVVP 5
Db 1 DEVVP 5

RESULT 8
AAB6377

ID AAB6377 standard; peptide; 6 AA.

AC AAB6377;

DT 09-APR-2001 (first entry)

DE Hepatitis C virus protease inhibitor boronic acid peptide #23.

KW Hepatitis C virus; protease; boronic acid; inhibitor; liver cirrhosis;

KW liver cancer; NS3; antiviral agent.

OS Synthetic.

Key location/Qualifiers

FT /label= OTHER

FT /note= "optionally Boc-Asp(OTBu)"

```

FT  /label= OTHER
FT  /note= "optionally Glu(OcBu)"
FT  Modified-site
FT  /label= OTHER
FT  /note= "optionally borovinylgly pinanediol ester,
FT  borocyclopropylglycine pinanediol ester or
FT  borocyclopropylglycine pinanediol ester.Hcl"
XX  WO200102424-A2.
XX  11-JAN-2001.
XX  07-JUN-2000; 2000WO-US018655.
XX  07-JUL-1999; 99US-0142561P.
XX  (DUPO ) DU PONT PHARM CO.
XX  Kettner CA, Jagannathan S, Forsyth TP;
XX  WPI; 2001-103001/11.
XX  New boronic acid derivatives, optionally containing peptides, used to
XX  treat hepatitis C infections, are hepatitis C viral protease inhibitors.
XX  Example 15; Page 132; 258pp; English.
XX  The present invention provides a number of boronic acid derivatives which
XX  act as inhibitors of the hepatitis C virus NS3 protease enzyme. They can
XX  be used to treat infection by the virus, which can cause liver cirrhosis
XX  and liver cancer
XX  Sequence 6 AA;
SQ
Query Match 100.0%; Score 26; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DEVVP 5
Db 1 DEVVP 5
RESULT 9
AAB6384
ID AAB6384 standard; peptide; 6 AA.
XX
AC AAB6384;
XX
DT 09-APR-2001 (first entry)
XX
DE Hepatitis C virus protease inhibitor boronic acid peptide #30.
XX
KM Hepatitis C virus; protease; boronic acid; inhibitor; liver cirrhosis;
XX  liver cancer; NS3; antiviral agent.
XX
OS Synthetic.
XX
XX Key
XX  Location/Qualifiers
XX  1
XX  /label= OTHER
XX  /note= "optionally Boc-Asp(OcBu)"
XX
FT Modified-site
FT  /label= OTHER
FT  /note= "optionally Glu(OcBu)"
XX
FT Modified-site
FT  /label= OTHER
FT  /note= "optionally boroser(OBz1) pinanediol,
FT  boroser(OBz1)-ClOH16, boroser pinanediol, boroser(OBz1)
FT  pinanediol Hcl or boroser pinanediol Hcl"
XX
XX WO200102424-A2.

```

```

PD 11-JAN-2001.
XX
XX 07-JUN-2000; 2000WO-US018655.
XX
XX 07-JUL-1999; 99US-0142561P.
XX
XX (DUPO ) DU PONT PHARM CO.
XX
XX Kettner CA, Jagannathan S, Forsyth TP;
XX  WPI; 2001-103001/11.
XX
XX New boronic acid derivatives, optionally containing peptides, used to
XX  treat hepatitis C infections, are hepatitis C viral protease inhibitors.
XX  Example 46; Page 154; 258pp; English.
XX
XX The present invention provides a number of boronic acid derivatives which
XX  act as inhibitors of the hepatitis C virus NS3 protease enzyme. They can
XX  be used to treat infection by the virus, which can cause liver cirrhosis
XX  and liver cancer
XX  Sequence 6 AA;
SQ
Query Match 100.0%; Score 26; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DEVVP 5
Db 1 DEVVP 5
RESULT 10
AAG64159
ID AAG64159 standard; peptide; 6 AA.
XX
AC AAG64159;
XX
DT 19-OCT-2001 (first entry)
XX
DE HCV NS3 protease inhibitor.
XX
XX Hepatitis C virus; HCV; NS3 protease; alpha-ketoamide inhibitor;
XX  virucide; hepatotropic; antiinflammatory; viral infection.
XX
OS Synthetic.
XX
XX Key
XX  Location/Qualifiers
XX  6
XX  /label= "boroa1g"
XX
FT Modified-site
FT  /note= "boroa1g"
XX
XX WO200140262-A1.
XX
XX 07-JUN-2001.
XX
XX 01-DEC-2000; 2000WO-US032677.
XX
XX 03-DEC-1999; 99US-0168998P.
XX
XX (DUPO ) DU PONT PHARM CO.
XX
XX Han W;
XX
XX WPI; 2001-464936/50.
XX
XX New ketoamide derivatives useful for treating infections e.g. hepatitis C
XX  virus.
XX
XX Disclosure; Page 195; 282pp; English.
XX
XX The invention relates to novel ketoamide and ketoester derivatives for
XX  use as inhibitors of hepatitis C virus (HCV) NS3 protease inhibitors. The
XX

```


SQ Sequence 6 AA;

Query Match 100.0%; Score 26; DB 5; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVVP 5
 |||||
 DB 1 DEVVP 5

RESULT 13

ABG31915

ID ABG31915 standard; peptide; 6 AA.

AC ABG31915;

XX 05-NOV-2002 (first entry)

XX HCV serine protease imidazolidinone inhibitor #1.

XX HCV; hepatitis C; imidazolidinone; serine protease inhibitor; virucide;

XX hepatotropic; antiinflammatory; NS3 protease; growth inhibitor;

XX viral infection; blood plasma processing.

XX Synthetic.

XX Key

XX Modified-site

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

SQ Sequence 6 AA;

Query Match 100.0%; Score 26; DB 5; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVVP 5
 |||||
 DB 1 DEVVP 5

RESULT 14

ABB05374

ID ABB05374 standard; peptide; 6 AA.

AC ABB05374;

XX 08-APR-2002 (first entry)

XX Peptide Q9714.

XX Hepatitis C virus; HCV; hepatitis C protease NS3; inhibitor; nootropic;

XX neuroprotective; tranquilizer; anticonvulsant; virucide; hepatotropic;

XX antiinflammatory; hepatitis C infection; neurological disorder; epilepsy;

XX anxiety; insomnia; Alzheimer's disease.

XX Synthetic.

XX Key

XX Modified-site

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

SQ Sequence 6 AA;

Query Match 100.0%; Score 26; DB 5; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVVP 5
 |||||
 DB 1 DEVVP 5

Disclosure; Page 17; 46pp; English.

XX The present invention describes a binding site (I) of hepatitis C
 CC protease (NS3):NS4A complex characterized by binding of a sequence (S),
 CC where binding is inhibitory when measured by enzymatic hydrolysis of a
 CC peptide substrate encompassing P6-P7' binding sites, and non-inhibitory
 CC when measured by enzymatic hydrolysis of a peptide substrate encompassing
 CC P6-P2' binding sites but does not extend into P4'-P7' binding sites
 CC region. (I) has nootropic, neuroprotective, tranquilizer, virucide,
 CC anticonvulsant, hepatotropic and antiinflammatory activities. (I) is
 CC useful for the discovery of inhibitors of hepatitis C protease and the
 CC treatment of hepatitis C disease. Inhibitors of hepatitis C can also be
 CC used for treating neurological disorders related to modulation of a
 CC potassium channel, more specifically the M-current, formed by expression
 CC of KCNQ2 and KCNQ3 genes, such as epilepsy, anxiety, insomnia or
 CC Alzheimer's disease. The present sequence represents a peptide which is
 CC used in the exemplification of the present invention

WPI; 2002-154599/20.

Kettner CA, Hixon MS;

(DUPONT) DUPONT PHARM CO.

11-JUN-2000; 2000US-0210900P.

08-JUN-2001; 2001WO-US018751.

20-DEC-2001.

WO200196540-A2.

Location/Qualifiers

/label= OTHER

/note= "OTHER=Hydrogenated"

/label= OTHER

/note= "OTHER= L-2-amino-4-pentonic acid- boronic acid-
 pinane diol ester-trifluoroacetate"

MO200248157-A2.

20-JUN-2002.

12-DEC-2001; 2001WO-US047916.

13-DEC-2000; 2000US-0255168P.

(BRIM) BRISTOL MYERS SQUIBB PHARMA CO.

Han Q;

WPI; 2002-599498/64.

New imidazolidinones useful as serine protease inhibitors in the
 treatment of e.g. viral infection.

Example 20; Page 115; 173pp; English.

XX This invention relates to novel imidazolidinones or their stereoisomers,
 CC salts or prodrugs which are useful as serine protease inhibitors. The
 CC imidazolidinones of the invention may have virucide, hepatotropic, or
 CC antiinflammatory activities and may be used as a serine protease
 CC inhibitor (preferably Hepatitis C virus (HCV) NS3 protease inhibitor) or
 CC a HCV growth inhibitor. Compounds of the invention are useful for
 CC treating viral infection e.g. hepatitis C virus (HCV) infection and as a
 CC reagent used as inhibitors of HCV protease in the processing of blood
 CC plasma for diagnostic and other commercial purposes. The imidazolidinones
 CC of the invention inhibit HCV NS3 protease and/or HCV growth and thus can
 CC be used in the blood plasma assay. The present sequence represents a
 CC imidazolidinone protease inhibitor shown in the examples of the
 CC specification

| | |
|-----------------------|---|
| RESULT 15 | |
| ABG32506 | |
| ID | ABG32506 standard; peptide; 6 AA. |
| XX | |
| AC | ABG32506; |
| XX | |
| DT | 15-NOV-2002 (first entry) |
| XX | |
| DE | Peptide inhibitor for HCV NS3 protease. |
| XX | |
| KM | NS3; HCV; protease; HCV infection; hepatitis; cirrhosis; liver cancer; |
| KM | pyrimidinone; serine protease inhibitor; vtrucide; hepatotropic; |
| XX | antiinflammatory; blood plasma processing. |
| XX | |
| OS | Synthetic. |
| XX | |
| FH | Key |
| FT | Modified-site |
| FT | Location/Qualifiers |
| FT | /note= "asp is hydrogenated" |
| FT | Modified-site |
| FT | 6 |
| FT | /note= "BoroAlg residue" |
| PN | |
| XX | WO200248116-A2. |
| XX | |
| PD | 20-JUN-2002. |
| XX | |
| XX | |
| PF | 12-DEC-2001; 2001WO-US047911. |
| XX | |
| PR | 13-DEC-2000; 2000US-0255290P. |
| XX | |
| PA | (BRIM) BRISTOL-MYERS SQUIBB PHARMA CO. |
| XX | |
| PI | Glunz PW, Douty BD, Han W; |
| XX | |
| DR | WPI; 2002-627251/67. |
| XX | |
| XX | |
| PT | New pyrimidiones useful as serine protease inhibitors in the treatment |
| PT | of e.g. viral infection. |
| XX | |
| ES | Example 140; Page 191; 270pp; English. |
| XX | |
| CC | |
| CC | The invention relates to pyrimidiones of a formula given in the claims |
| CC | of the specification, their stereoisomers, salts and produgs. In assays, |
| CC | the pyrimidinone compounds inhibited Hepatitis C virus (HCV) NS3 protease |
| CC | with IC ₅₀ values of less than 100 micro M. The compounds are useful for |
| CC | treating viral infection e.g. HCV infection (the causative agent of acute |
| CC | hepatitis and associated with cirrhosis and liver cancer) and as a |
| CC | reagent used as inhibitors of HCV protease in the processing of blood |
| CC | plasma for diagnostic and other commercial purposes. The present sequence |
| CC | is a peptide inhibitor used to determine NS3 concentration in assays |
| CC | described in the specification |
| XX | |
| SO | Sequence 6 AA; |
| | |
| Query Match | 100.0%; Score 26; DB 5; Length 6; |
| Best Local Similarity | 100.0%; Pred. No. 1,7e+06; |
| Matches | 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| | |
| OY | 1 DEVVP 5 |
| | |
| | 1 DEVVP 5 |
| | db |

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Search completed: December 8, 2004, 08:54:39
Job time : 162 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using SW model

Run on: December 8, 2004, 08:30:16 ; Search time 149 Seconds
(without alignments)
12.038 Million cell updates/sec

Title: SEQ1
Perfect score: 26
Sequence: 1 deerp 5

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 43520

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | ID | Description |
|------------|-------|--------------------|--------------|--------------------|
| 1 | 26 | 100.0 | 5 4 AAB66374 | Aab66374 Hepatitis |
| 2 | 26 | 100.0 | 5 5 ABG31916 | ABG31916 HCV serin |
| 3 | 26 | 100.0 | 5 7 ABU61522 | ABU61522 Hepatitis |
| 4 | 26 | 100.0 | 5 7 ABU61519 | ABU61519 Hepatitis |
| 5 | 21 | 80.8 | 5 4 AAB66355 | Aab66355 Hepatitis |
| 6 | 20 | 76.9 | 4 4 AAM52537 | Aam52537 NS3 prote |
| 7 | 20 | 76.9 | 4 4 AAB66375 | Aab66375 Hepatitis |
| 8 | 20 | 76.9 | 4 5 ABG31917 | ABG31917 HCV serin |
| 9 | 20 | 76.9 | 4 5 ABG31918 | ABG31918 HCV serin |
| 10 | 20 | 76.9 | 5 4 AAB66364 | Aab66364 Hepatitis |
| 11 | 20 | 76.9 | 5 7 ABU61524 | ABU61524 Hepatitis |
| 12 | 19 | 73.1 | 4 2 AAR44221 | Aar44221 Tyrosinas |
| 13 | 19 | 73.1 | 4 2 AAR58582 | Aar58582 N termina |
| 14 | 19 | 73.1 | 4 4 AAB66373 | Aab66373 Hepatitis |
| 15 | 18 | 69.2 | 4 4 AAM73297 | Aam73297 H160 cell |
| 16 | 18 | 69.2 | 5 8 ADO70448 | ADO70448 Trp-conta |
| 17 | 17 | 65.4 | 4 2 AAR44222 | Aar44222 Tyrosinas |
| 18 | 17 | 65.4 | 4 2 AAR58583 | Aar58583 Protein t |
| 19 | 17 | 65.4 | 5 3 AAB33073 | Aab33073 Protein t |
| 20 | 17 | 65.4 | 5 8 AAB36741 | Aab36741 N-termina |
| 21 | 17 | 65.4 | 5 8 ADO70480 | ADO70480 Trp-conta |
| 22 | 17 | 65.4 | 5 8 AAR65523 | Aar65523 Endotheli |
| 23 | 16 | 61.5 | 5 2 AAY15685 | Aay15685 Peptide u |
| 24 | 16 | 61.5 | 5 3 AAY80839 | Aay80839 Fluoropho |
| 25 | 16 | 61.5 | 5 3 AAY80839 | Aay80839 Fluoropho |

| | | | | |
|----|----|------|--------------|--------------------|
| 26 | 16 | 61.5 | 5 4 AAG66393 | Aag66393 Azapeptid |
| 27 | 16 | 61.5 | 5 8 ADO70478 | ADO70478 Trp-conta |
| 28 | 15 | 57.7 | 4 2 AAR48289 | Aar48289 ACE inhib |
| 29 | 15 | 57.7 | 4 2 AAR88260 | Aar88260 Intermedi |
| 30 | 15 | 57.7 | 4 2 AAR88264 | Aar88264 Intermedi |
| 31 | 15 | 57.7 | 4 2 AAR88263 | Aar88263 Intermedi |
| 32 | 15 | 57.7 | 4 2 AAR88262 | Aar88262 Intermedi |
| 33 | 15 | 57.7 | 4 2 AAR88261 | Aar88261 Intermedi |
| 34 | 15 | 57.7 | 4 2 AAR88266 | Aar88266 Intermedi |
| 35 | 15 | 57.7 | 4 2 AAW93984 | Aaw93984 Antineopl |
| 36 | 15 | 57.7 | 4 2 AAW93985 | Aaw93985 Antineopl |
| 37 | 15 | 57.7 | 4 2 AAW62500 | Aaw62500 ICE pepti |
| 38 | 15 | 57.7 | 4 2 AAW76200 | Aaw76200 Mouse cas |
| 39 | 15 | 57.7 | 4 2 AAW52756 | Aaw52756 Aminometh |
| 40 | 15 | 57.7 | 4 2 AAW48940 | Aaw48940 Apopain (|
| 41 | 15 | 57.7 | 4 2 AAW66735 | Aaw66735 Dolastaci |
| 42 | 15 | 57.7 | 4 2 AAW56305 | Aaw56305 Peptide c |
| 43 | 15 | 57.7 | 4 2 AAW48948 | Aaw48948 Apopain (|
| 44 | 15 | 57.7 | 4 2 AAW65566 | Aaw65566 Peptide u |
| 45 | 15 | 57.7 | 4 2 AAW65566 | Aaw65566 Peptide u |

ALIGNMENTS

| | | |
|----------|---|---|
| RESULT 1 | AAB66374 | standard; peptide; 5 AA. |
| XX | XX | XX |
| AC | AAB66374; | |
| XX | XX | XX |
| DT | 09-APR-2001 (first entry) | |
| XX | XX | XX |
| DE | Hepatitis C virus protease inhibitor boronic acid peptide #20. | |
| XX | XX | XX |
| KW | Hepatitis C virus; protease; boronic acid; inhibitor; liver cirrhosis; | |
| KM | liver cancer; NS3; antiviral agent. | |
| XX | XX | XX |
| OS | Synthetic. | |
| XX | XX | XX |
| FH | Key | Location/Qualifiers |
| FT | Modified-site | 1 /label= OTHER |
| FT | FT | /note= "optionally Boc-Asp(OtBu) or Ac-Asp(OtBu)" |
| FT | Modified-site | 2 /label= OTHER |
| FT | FT | /note= "Glu(OtBu)" |
| XX | XX | XX |
| PN | W0200102424-A2. | |
| XX | XX | XX |
| PD | 11-JAN-2001. | |
| XX | XX | XX |
| PP | 07-JUL-2000; 2000WO-US018655. | |
| XX | XX | XX |
| PR | 07-JUL-1999; 99US-0142561P. | |
| XX | XX | XX |
| PA | (DUPO) DU PONT PHARM CO. | |
| XX | XX | XX |
| PI | Kettner CA, Jagannathan S, Forsyth TP; | |
| XX | XX | XX |
| DR | WPI; 2001-103001/11. | |
| XX | XX | XX |
| PT | New boronic acid derivatives, optionally containing peptides, used to | |
| XX | XX | XX |
| PS | treat hepatitis C infections, are hepatitis C viral protease inhibitors. | |
| XX | XX | XX |
| XX | Example 9: Page 127; 258pp; English. | |
| XX | XX | XX |
| CC | The present invention provides a number of boronic acid derivatives which | |
| CC | act as inhibitors of the hepatitis C virus NS3 protease enzyme. They can | |
| CC | be used to treat infection by the virus, which can cause liver cirrhosis | |
| CC | and liver cancer | |
| XX | XX | XX |
| SQ | Sequence 5 AA; | |

Query Match 100.0%; Score 26; DB 4; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5
 |||||
 DB 1 DEVP 5

RESULT 2
 ABG31916
 ID ABG31916 standard; peptide; 5 AA.

XX AC ABG31916;

XX DT 05-NOV-2002 (first entry)

XX DE HCV serine protease imidazolidinone inhibitor #2.

XX KM HCV; hepatitis C; imidazolidinone; serine protease inhibitor; virucide;
 XX KW hepatotropic; antiinflammatory; NS3 protease; growth inhibitor;
 XX KM viral infection; blood plasma processing.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Modified-site 1 /label= OTHER

FT Misc-difference 2 /note= "OTHER= Boc-Asp(OtBu)"

FT Modified-site 5 /note= "Glu(OtBu)"

FT /label= OTHER

FT /note= "OTHER= Hydroxyl group"

XX PN W0200248157-A2.

XX PD 20-JUN-2002.

XX PF 12-DEC-2001; 2001WO-US047916.

XX PR 13-DEC-2000; 2000US-0255168P.

XX PA (BRIM) BRISTOL MYERS SQUIBB PHARMA CO.

XX PI Han Q;

XX DR WPI; 2002-599498/64.

XX PT New imidazolidinones useful as serine protease inhibitors in the
 PT treatment of e.g. viral infection.

XX PS Example 20; Page 115; 173pp; English.

XX CC This invention relates to novel imidazolidinones or their stereoisomers,
 CC salts or prodrugs which are useful as serine protease inhibitors. The
 CC imidazolidinones of the invention may have virucide, hepatotropic, or
 CC antiinflammatory activities and may be used as a serine protease
 CC inhibitor (preferably Hepatitis C virus (HCV) NS3 protease inhibitor) or
 CC a HCV growth inhibitor. Compounds of the invention are useful for
 CC treating viral infection e.g. hepatitis C virus (HCV) infection and as a
 CC reagent used as inhibitors of HCV protease in the processing of blood
 CC plasma for diagnostic and other commercial purposes. The imidazolidinones
 CC of the invention inhibit HCV NS3 protease and/or HCV growth and thus can
 CC be used in the blood plasma assay. The present sequence represents a
 CC imazolidinone protease inhibitor shown in the examples of the
 CC specification

XX SQ Sequence 5 AA;

Query Match 100.0%; Score 26; DB 5; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5
 |||||
 DB 1 DEVP 5

RESULT 3
 ABU61522
 ID ABU61522 standard; peptide; 5 AA.

XX AC ABU61522;

XX DT 08-AUG-2003 (first entry)

XX DE Hepatitis C virus NS3 protease inhibitor peptide.

XX KM Hepatitis C virus; NS3 protease; hepatotropic; virucide;
 XX KW antiinflammatory; serine protease inhibitor; hepatitis C virus;
 XX KM NS3 Protease Inhibitor; viral infection; elastase; chymotrypsin.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Modified-site 1 /label= O-tBu (not defined)

FT Modified-site 1 /note= "Boc (not defined)"

FT Modified-site 2 /note= "O-tBu (not defined)"

FT Modified-site 5 /note= "C-terminal hydroxyl"

XX PN US2002177725-A1.

XX PD 28-NOV-2002.

XX PF 28-OCT-2001; 2001US-00039317.

XX PR 23-OCT-2000; 2000US-0242557P.

XX PA (PRIE/) PRIESTLEY E S.

XX PI Priestley ES;

XX DR WPI; 2003-465950/44.

XX PT New class of peptides are inhibitors of hepatitis C virus NS3 protein,
 PT useful for treating e.g. hepatitis.

XX PS Example 1; Page 27; 54pp; English.

XX CC The invention describes novel peptide useful for treating viral
 CC infections e.g. Hepatitis C virus (HCV) infections. The compounds have
 CC HCV NS3 protease inhibitory selectivity over inhibition of elastase and
 CC chymotrypsin. This is the amino acid sequence of a modified peptide
 CC associated with an assay of NS3 protease activity

XX SQ Sequence 5 AA;

Query Match 100.0%; Score 26; DB 7; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5
 |||||
 DB 1 DEVP 5

RESULT 4
 ABU61519
 ID ABU61519 standard; peptide; 5 AA.

| | | |
|---------------|---|---------------|
| AC | ABU61519; | |
| XX | | |
| DT | 08-AUG-2003 | (first entry) |
| XX | | |
| DE | Hepatitis C virus NS3 protease inhibitor. | |
| XX | | |
| KW | Hepatitis C virus; NS3 protease; hepatotropic; virucide; antiinflammatory; serine protease inhibitor; hepatitis C virus; NS3 Protease Inhibitor; viral infection; elastase; chymotrypsin. | |
| XX | | |
| OS | Synthetic. | |
| XX | | |
| Key | Location/Qualifiers | |
| Modified-site | 5 | |
| FT | /note= "(1R)-1-amino-3-phenylpropylboronic acid (+)- | |
| FT | pinanediol ester, or (1R)-1-amino-4-phenylbutylboronic | |
| FT | acid (+)-pinanediol ester, (1R)-amino-5- | |
| FT | phenylbutylboronic acid (+)- pinanediol ester, or (1R)-1- | |
| FT | amino-3-(2- naphthyl)propylboronic acid (+)-pinanediol | |
| FT | ester, or (1R)-1-amino-3-(2-methyl phenyl)propylboronic | |
| FT | acid (+)-pinanediol ester, or (1R)-1-amino-3-(3- | |
| FT | methyl)phenylpropylboronic acid (+)-pinanediol ester, or | |
| FT | (1R)-1-amino-3-(4-methyl)phenylpropylboronic acid (+)- | |
| FT | pinanediol ester, or (1R)-1-amino-3-(1,1'- biphényl)-4- | |
| FT | ylpropylboronic acid (+)- pinanediol ester, or (1R)-1- | |
| FT | amino-3-(2,5-dimethyl) phenylpropylboronic acid (+)- | |
| FT | pinanediol ester, or (1R)-1-amino-3-(2,4- | |
| FT | dimethyl)phenylpropylboronic acid (+)-pinanediol ester, or | |
| FT | (1R)-1-amino-3-(4- trifluoromethyl)phenylpropylboronic | |
| FT | acid (+) pinanediol ester, or (1R)-1-amino-3-(3- | |
| FT | trifluoromethyl)phenylpropylboronic acid (+)- pinanediol | |
| FT | ester, or (1R)-1-amino-3-(4-fluoro) phenylpropylboronic | |
| FT | acid (+) pinanediol ester, or (1R)-1-amino-3- | |
| FT | (4phenoxy)phenylpropylboronic acid (+)-pinanediol ester, | |
| FT | or (1R)-1-amino-3-(4- isopropyl)phenylpropylboronic acid | |
| FT | (+)-pinanediol ester, or (1R)-1-amino-3-(4-cyclohexyl) | |
| FT | phenylpropylboronic acid (+)- pinanediol ester, or (1R)-1- | |
| FT | amino-3-(4-tert-butyl) phenylpropylboronic acid (+)- | |
| FT | pinanediol ester, or (1R)-1-amino-3-(4- | |
| FT | methoxy)phenylpropylboronic acid (+)-pinanediol ester, or | |
| FT | (1R)-1-amino-3-(4- chloro)phenylpropylboronic acid (+)- | |
| FT | pinanediol ester, or (1R)-1-amino-3-(4-bromo) | |
| FT | phenylpropylboronic acid (+)-pinanediol ester, or (1R)-1- | |
| FT | amino-3-(2-fluoro)phenylpropylboronic acid (+)-pinanediol | |
| FT | ester, or (1R)-1-amino-3-(3-fluoro)phenylpropylboronic | |
| FT | acid (+)-pinanediol ester, or (1R)-1-amino-3-(2,6- | |
| FT | difluoro) phenylpropylboronic acid (+)- pinanediol ester, | |
| FT | or (1R)-1-amino-3-(4-hydroxy)phenylpropylboronic acid (+)- | |
| FT | pinanediol ester, or (1R)-1- amino-5-methylhexylboronic | |
| FT | acid (+)- pinanediol ester, or (1R)-1-amino-5-methylhexylboronic | |
| FT | acid (+)- pinanediol ester, or (1R)-1-amino-4- | |
| FT | cyclobutylbutylboronic acid (+)-pinanediol ester, or (1R) | |
| FT | -1-amino-5-ethylheptylboronic acid (+)- pinanediol ester | |
| FT | 1R is not defined." | |
| XX | | |
| US | US2002177725-A1. | |
| XX | | |
| PD | 28-NOV-2002. | |
| XX | | |
| PF | 28-OCT-2001; 2001US-00039317. | |
| XX | | |
| PR | 23-OCT-2000; 2000US-0242557P. | |
| XX | | |
| PA | (PRIE/) PRIESTLEY E S. | |
| PI | Priestley ES; | |
| XX | | |
| DR | WPI: 2003-465950/44. | |
| XX | | |
| PT | New class of peptides are inhibitors of hepatitis C virus NS3 protein, | |
| PT | useful for treating e.g. hepatitis. | |

| | |
|----------|---|
| PS | Example; Page 14-15; 54pp; English. |
| XX | The invention describes novel peptide useful for treating viral |
| CC | infections e.g. Hepatitis C virus (HCV) infections. The compounds have |
| CC | HCV NS3 protease inhibitory selectivity over inhibition of elastase and |
| CC | chymotrypsin. This is the amino acid sequence of a modified peptide that |
| CC | functions as an NS3 inhibitor |
| XX | |
| SQ | Sequence 5 AA; |
| OY | Query Match 100.0%; Score 26; DB 7; Length 5; Best Local Similarity 100.0%; Pred. No. 1.7e+06; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| Db | 1 DEVP 5 1 DEVP 5 |
| RESULT 5 | |
| AAB66355 | ID AAB66355 standard; peptide; 5 AA. |
| XX | |
| AC | AAB66355; |
| XX | |
| XX | 09-APR-2001 (first entry) |
| DT | |
| XX | Hepatitis C virus protease inhibitor boronic acid peptide #5. |
| DX | |
| DE | Hepatitis C virus; protease; boronic acid; inhibitor; liver cirrhosis; |
| KM | liver cancer; NS3; antiviral agent. |
| XX | |
| OS | Synthetic. |
| XX | |
| FH | Key Location/Qualifiers |
| FT | Modified-site 3 /label= OTHER |
| FT | /note= "2-methyl-phenylalanine" |
| FT | Modified-site 4 /label= OTHER |
| FT | /note= "3-methyl-valine" |
| XX | |
| XX | MO200102424-A2. |
| XN | |
| PD | 11-JAN-2001. |
| XX | |
| PJ | 07-JUL-2000; 2000WO-US018655. |
| PR | 07-JUL-1999; 99US-0142561P. |
| XX | |
| PA | (DUPO) DU PONT PHARM CO. |
| XX | |
| PI | Ketner CA, Jagannathan S, Forsyth TP; |
| DR | WPI, 2001-103001/11. |
| XX | |
| PT | New boronic acid derivatives, optionally containing peptides, used to |
| PR | treat hepatitis C infections, are hepatitis C viral protease inhibitors. |
| XX | |
| PS | Claim 8; Page 11; 258pp; English. |
| XX | |
| CC | The present invention provides a number of boronic acid derivatives which |
| CC | act as inhibitors of the hepatitis C virus NS3 protease enzyme. They can |
| CC | be used to treat infection by the virus, which can cause liver cirrhosis |
| CC | and liver cancer |
| XX | |
| SQ | Sequence 5 AA; |
| OY | Query Match 80.8%; Score 21; DB 4; Length 5; Best Local Similarity 80.0%; Pred. No. 1.7e+06; Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0; |

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Db          1 DEFPV 5
|||
RESULT 6
ID AAM52537
XX AAM52537 standard; peptide; 4 AA.
XX
AC AAM52537;
XX
DT 31-JAN-2002 (first entry)
XX
DE NS3 protease peptide inhibitor #2.
XX
KM Virucide; pyrrolopyrazinone derivative; Hepatitis C virus inhibitor;
XX nonstructural 3 protease; NS3 protease; viral infection.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note="Optionally Z-Glu(OtBu) or H-Glu(OtBu)"
FT Modified-site 4 /note="Optionally Pro-OBzl or Pro-Or"
XX
PN MO200164678-A2.
XX
PD 07-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US006269.
XX
PR 29-FEB-2000; 2000US-0185618P.
XX
PA (DUPO ) DUPONT PHARM CO.
XX
PI Zhang X, Han W;
XX
DR WPI; 2001-656752/75.
XX
FT New pyrrolopyrazinone derivatives useful for treating Hepatitis C virus
PT infection are NS3 protease inhibitors.
XX
PS Disclosure; Page 134; 191pp; English.
XX
CC The present invention relates to a novel pyrrolopyrazinone derivative,
CC its stereoisomer or salt. It was found that the derivative is a Hepatitis
CC C virus (HCV) nonstructural (NS) 3 protease inhibitor. The derivative is
CC useful for the manufacture of a medicament for the treatment of HCV and
CC in therapy for treating HCV infection. The present peptide is a peptide
CC inhibitor for HCV NS3 protease, which was used to illustrate the present
CC invention
XX
SQ Sequence 4 AA;
Query Match 76.9%; Score 20; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 EVVP 5
Db 1 EVVP 4
|||
RESULT 7
ID AAB66375
XX AAB66375 standard; peptide; 4 AA.
XX
AC AAB66375;
XX
DT 09-APR-2001 (first entry)
XX
DE Hepatitis C virus protease inhibitor boronic acid peptide #21.
XX

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KM Hepatitis C virus; protease; boronic acid; inhibitor; liver cirrhosis;
XX liver cancer; NS3; antiviral agent.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /label= OTHER
FT Modified-site 4 /note="Optionally Glu(OtBu) or Ac-Glu(OtBu)"
XX
PN MO200102424-A2.
XX
PD 11-JAN-2001.
XX
PF 07-JUL-2000; 2000WO-US018655.
XX
PR 07-JUL-1999; 99US-0142561P.
XX
PA (DUPO ) DU PONT PHARM CO.
XX
PI Kettner CA, Jagannathan S, Forsyth TP;
XX
DR WPI; 2001-103001/11.
XX
PT New boronic acid derivatives, optionally containing peptides, used to
PT treat hepatitis C infections, are hepatitis C viral protease inhibitors.
XX
PS Example 9; Page 128; 256pp; English.
XX
CC The present invention provides a number of boronic acid derivatives which
CC act as inhibitors of the hepatitis C virus NS3 protease enzyme. They can
CC be used to treat infection by the virus, which can cause liver cirrhosis
CC and liver cancer
XX
SQ Sequence 4 AA;
Query Match 76.9%; Score 20; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 EVVP 5
Db 1 EVVP 4
|||
RESULT 8
ID ABG31917
XX ABG31917 standard; peptide; 4 AA.
XX
AC ABG31917;
XX
DT 05-NOV-2002 (first entry)
XX
DE HCV serine protease imidazolinone inhibitor #3.
XX
KM HCV; hepatitis C; imidazolidinone; serine protease inhibitor; virucide;
XX hepatotropic; antiinflammatory; NS3 protease; growth inhibitor;
XX viral infection; blood plasma processing.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1 /note="Glu(OtBu)"
FT Modified-site 1 /label= OTHER
FT Modified-site 4 /note="OTHER= Hydrogenated"
FT Modified-site 4 /label= OTHER
FT /note="OTHER= Hydroxy] group"
XX
PN MO200248157-A2.
XX

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XX PD 20-JUN-2002.
XX PF 12-DEC-2001; 2001WO-US047916.
XX PR 13-DEC-2000; 2000US-0255168P.
XX XX
XX PA (BRIM ) BRISTOL MYERS SQUIBB PHARMA CO.
XX PT
XX PR Han Q;
XX DR WPI; 2002-599498/64.
XX XX
XX PT New imidazolidinones useful as serine protease inhibitors in the
XX PT treatment of e.g. viral infection.
XX PS
XX PS Example 20; Page 117; 173pp; English.
XX XX
XX CC This invention relates to novel imidazolidinones or their stereoisomers,
XX CC salts or prodrugs which are useful as serine protease inhibitors. The
XX CC imidazolidinones of the invention may have virucide, hepatotropic, or
XX CC antiinflammatory activities and may be used as a serine protease
XX CC inhibitor (preferably Hepatitis C virus (HCV) NS3 protease inhibitor) or
XX CC a HCV growth inhibitor. Compounds of the invention are useful for
XX CC treating viral infection e.g. hepatitis C virus (HCV) infection and as a
XX CC reagent used as inhibitors of HCV protease in the processing of blood
XX CC plasma for diagnostic and other commercial purposes. The imidazolidinones
XX CC of the invention inhibit HCV NS3 protease and/or HCV growth and thus can
XX CC be used in the blood plasma assay. The present sequence represents a
XX CC imidazolidione protease inhibitor shown in the examples of the
XX CC specification
XX SQ
XX SQ Sequence 4 AA;
XX
XX Query Match 76.9%; Score 20; DB 5; Length 4;
XX Best Local Similarity 100.0%; Pred.No. 1.7e+06;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
XX QY 2 EVVP 5
XX ||||
XX Db 1 EVVP 4
XX
XX RESULT 9
XX ABG31918
XX ID ABG31918 standard; peptide; 4 AA.
XX XX
XX AC ABG31918;
XX DT 05-NOV-2002 (first entry)
XX DE
XX DE HCV serine protease imidazolidinone inhibitor #4.
XX XX
XX HCV; hepatitis C; imidazolidinone; serine protease inhibitor; virucide;
XX KW hepatotropic; antiinflammatory; NS3 protease; growth inhibitor;
XX KW viral infection; blood plasma processing.
XX OS
XX OS Synthetic.
XX FH
XX FH Key Location/Qualifiers
XX FT Modified-site 1
XX FT /label= "Z
XX FT /note= "2-Glu(OCBu)"
XX FT Modified-site 4
XX FT /note= "Pro-Obz1"
XX PN
XX PN WO200248157-A2.
XX PD
XX PD 20-JUN-2002.
XX XX
XX PF 12-DEC-2001; 2001WO-US047916.
XX PR
XX PR 13-DEC-2000; 2000US-0255168P.
XX XX

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| | |
|-----------------------|---|
| PA | (BRIM) BRISTOL MYERS SQUIBB PHARMA CO. |
| XX | |
| XX | Han Q; |
| XX | |
| DR | WPI; 2002-599498/64. |
| XX | |
| XX | New imidazolidinones useful as serine protease inhibitors in the |
| PT | treatment of e.g. viral infection. |
| XX | |
| PS | Example 20; Page 117; 173pp; English. |
| XX | |
| CC | This invention relates to novel imidazolidinones or their stereoisomers, |
| CC | salts or prodrugs which are useful as serine protease inhibitors. The |
| CC | imidazolidinones of the invention may have virucide, hepatotropic, or |
| CC | antiinflammatory activities and may be used as a serine protease |
| CC | inhibitor (preferably Hepatitis C virus (HCV) NS3 protease inhibitor) or |
| CC | a HCV growth inhibitor. Compounds of the invention are useful for |
| CC | treating viral infection e.g. hepatitis C virus (HCV) infection and as a |
| CC | reagent used as inhibitors of HCV protease in the processing of blood |
| CC | plasma for diagnostic and other commercial purposes. The imidazolidinones |
| CC | of the invention inhibit HCV NS3 protease and/or HCV growth and thus can |
| CC | be used in the blood plasma assay. The present sequence represents a |
| CC | imidazolidione protease inhibitor shown in the examples of the |
| CC | specification |
| XX | |
| SQ | Sequence 4 AA: |
| | |
| Query Match | 76.9%; Score 20; DB 5; Length 4; |
| Best Local Similarity | 100.0%; Pred. No. 1.7e+06; |
| Matches | 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0 |
| QY | 2 EYVP 5 |
| | |
| DB | 1 EYVP 4 |
| | |
| RESULT 10 | |
| AAB66364 | |
| ID | AAB66364 standard; peptide; 5 AA. |
| XX | |
| AC | AAB66364; |
| XX | |
| XX | |
| DT | 09-APR-2001 (first entry) |
| XX | |
| DE | Hepatitis C virus protease inhibitor boronic acid peptide #14. |
| XX | |
| XX | Hepatitis C virus; protease; boronic acid; inhibitor; liver cirrhosis; |
| KM | liver cancer; NS3; antiviral agent. |
| XX | |
| OS | Synthetic. |
| XX | |
| PH | Key |
| FT | Modified-site |
| FT | 1 Location/Qualifiers |
| FT | /label=OTHER |
| FT | /note="C-terminal acetyl, optionally Glu(OtBu)" |
| FT | Modified-site |
| FT | 5 /label=OTHER |
| FT | /note="Optionally boro-L-2-amino-4-pentenoic acid |
| FT | (borolig) pinanediol or borolig-ClOH16" |
| PN | MO200102424-A2. |
| XX | |
| PD | 11-JAN-2001. |
| XX | |
| PF | 07-JUL-2000; 2000MO-US018655. |
| XX | |
| PR | 07-JUL-1999; 99US-0142561P. |
| XX | |
| PA | (DUPO) DU PONT PHARM CO. |
| XX | |
| PI | Kettner CA, Jagannathan S, Foreyth TE; |
| XX | |
| DR | WPI; 2001-103001/11. |


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PD 09-AUG-1994.
XX 09-APR-1992; 92JP-00089147.
PF 09-APR-1992; 92JP-00089147.
XX 09-APR-1992; 92JP-00089147.
PR 09-APR-1992; 92JP-00089147.
XX (SIYA ) SANSEI SEIYAKU KK.
PA
XX WPI; 1994-290910/36.
DR
XX New tyrosinase inhibitory peptide - for use in medicine, cosmetics and
XX agrochemicals.
PT
XX Claim 1; Page 2; 9pp; Japanese.
PS
XX AAR58582 is an N-terminal fragment of a tyrosinase inhibitory peptide.
CC The inhibitory peptide is useful in medicines, cosmetics, extraction from
CC agrochemicals, etc. It is prepared from known methods, eg. extraction from
CC a living body, synthetic methods, genetic recombination, etc. (see also
CC AAR58583)
XX
SQ Sequence 4 AA:

Query Match 73.1%; Score 19; DB 2; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 EVVP 5
   |||
   1 EIVP 4
Db

RESULT 14
AAB6373
ID AAB6373 standard; peptide; 4 AA.
XX
AC AAB6373;
XX
DT 09-APR-2001 (first entry)
XX
DE Hepatitis C virus protease inhibitor boronic acid peptide #19.
XX
KW Hepatitis C virus; protease; boronic acid; inhibitor; liver cirrhosis;
KW liver cancer; NS3; antiviral agent.
XX
OS Synthetic.
XX
PH Key Location/Qualifiers
FT Modified-site 1 /label= OTHER
FT /note= "Boc-Asp(OtBu) "
FT Modified-site 2 /label= OTHER
FT /note= "Glu(OtBu) "
XX
PN WO200102424-A2.
PD 11-JAN-2001.
XX
PF 07-JUL-2000; 2000WO-US018655.
XX
PR 07-JUL-1999; 99US-0142561P.
XX
PA (DUPO ) DU PONT PHARM CO.
XX
PI Kettner CA, Jagannathan S, Forsyth TP;
XX
DR WPI; 2001-103001/11.
XX
PT New boronic acid derivatives, optionally containing peptides, used to
PT treat hepatitis C infections, are hepatitis C viral protease inhibitors.
XX
PS Example 7; Page 123; 258pp; English.

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XX The present invention provides a number of boronic acid derivatives which
CC act as inhibitors of the hepatitis C virus NS3 protease enzyme. They can
CC be used to treat infection by the virus, which can cause liver cirrhosis
CC and liver cancer
XX
SQ Sequence 4 AA:

Query Match 73.1%; Score 19; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVV 4
   |||
   1 DEVV 4
Db

RESULT 15
AAW73297
ID AAW73297 standard; peptide; 4 AA.
XX
AC AAW73297;
XX
DT 08-FEB-1999 (first entry)
XX
DE HL60 cell line protein fragment.
XX
KW HL60; human; staurosporine; neurodegenerative disease; neuropathy;
KW immunodeficiency; geriatric disease; transplant rejection; therapy;
KW hyperproliferative disease; autoimmune disease; dermatological disease.
XX
OS Homo sapiens.
XX
PN WO9845429-A2.
XX
PD 15-OCT-1998.
XX
PF 14-APR-1998; 98WO-EP002157.
XX
PR 10-APR-1997; 97GB-00007307.
XX
PA (NOVS ) NOVARTIS AG.
PA (NOVS ) NOVARTIS-ERFINDUNGEN VERM GES MBH.
XX
PI Imfeld D, Fuerst P, Schindler P, Maerki W;
XX
DR WPI; 1998-568349/48.
XX
XX Polypeptides from the HL60 cell line - used to treat neurodegenerative
XX diseases e.g. neuropathies, immunodeficiencies, geriatric disease.
XX
PS Example 7; Page 30; 50pp; English.
XX
CC This sequence represents a fragment of a polypeptide of the invention.
CC The polypeptides were isolated from the HL60 cell line. The polypeptide
CC can be used as a drug, or as a marker or surrogate marker for monitoring
CC a cellular condition or disease achievable by application of
CC staurosporine. They can also be used for identification of a drug for
CC treatment of a disease selected from disease responsive to induction of a
CC cellular condition achievable by application of staurosporine, and
CC diseases responsive to inhibition of a cellular condition achievable by
CC application of staurosporine. The diseases include neurodegenerative
CC diseases, neuropathies, immunodeficiencies, geriatric disease, transplant
CC rejection diseases, hyperproliferative diseases, autoimmune diseases and
CC dermatological diseases
XX
SQ Sequence 4 AA:

Query Match 69.2%; Score 18; DB 2; Length 4;
Best Local Similarity 50.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 EVVP 5

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Wed Dec 8 10:04:34 2004

seq1.closed.rag

Page 8

DB 1 EIP 4

Search completed: December 8, 2004, 08:33:38
Job time : 152 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 8, 2004, 08:30:16 / Search time 37 Seconds
(without alignments)
8.962 Million cell updates/sec

Title: SEQ1
Perfect score: 26
Sequence: 1 decomp 5

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 476139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 26504

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/prodata/1/aa/5B.COMB.pep.*
3: /cgn2_6/prodata/1/aa/6A.COMB.pep.*
4: /cgn2_6/prodata/1/aa/6B.COMB.pep.*
5: /cgn2_6/prodata/1/aa/PCFUS.COMB.pep.*
6: /cgn2_6/prodata/1/aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------|
| 1 | 26 | 100.0 | 5 | 4 | US-10-015-328-8 |
| 2 | 26 | 100.0 | 5 | 4 | US-09-728-653-8 |
| 3 | 20 | 76.9 | 4 | 4 | US-10-015-328-9 |
| 4 | 20 | 76.9 | 4 | 4 | US-10-015-328-10 |
| 5 | 20 | 76.9 | 4 | 4 | US-09-728-653-9 |
| 6 | 20 | 76.9 | 4 | 4 | US-09-728-653-10 |
| 7 | 17 | 65.4 | 5 | 3 | US-09-020-880-41 |
| 8 | 17 | 65.4 | 5 | 3 | US-09-101-544-41 |
| 9 | 16 | 61.5 | 4 | 1 | US-08-335-198-21 |
| 10 | 16 | 61.5 | 5 | 3 | US-09-357-952-68 |
| 11 | 16 | 61.5 | 5 | 3 | US-09-521-650-68 |
| 12 | 16 | 61.5 | 5 | 3 | US-09-168-888-68 |
| 13 | 16 | 61.5 | 5 | 4 | US-09-947-387-68 |
| 14 | 16 | 61.5 | 5 | 4 | US-09-368-670C-10 |
| 15 | 16 | 61.5 | 5 | 4 | US-09-368-670C-34 |
| 16 | 15 | 57.7 | 4 | 1 | US-08-384-618-2 |
| 17 | 15 | 57.7 | 4 | 1 | US-08-446-925-9 |
| 18 | 15 | 57.7 | 4 | 1 | US-08-456-424-49 |
| 19 | 15 | 57.7 | 4 | 2 | US-08-800-007A-10 |
| 20 | 15 | 57.7 | 4 | 2 | US-09-146-331-9 |
| 21 | 15 | 57.7 | 4 | 2 | US-08-814-577-2 |
| 22 | 15 | 57.7 | 4 | 2 | US-08-915-414A-1 |
| 23 | 15 | 57.7 | 4 | 2 | US-08-896-885-9 |
| 24 | 15 | 57.7 | 4 | 3 | US-08-712-878-2 |
| 25 | 15 | 57.7 | 4 | 3 | US-09-226-568-39 |
| 26 | 15 | 57.7 | 4 | 3 | US-08-802-981-2 |
| 27 | 15 | 57.7 | 4 | 3 | US-08-802-981-3 |

| | | | | | | |
|----|----|------|---|---|-------------------|-------------------|
| 28 | 15 | 57.7 | 4 | 3 | US-08-802-981-177 | Sequence 177, App |
| 29 | 15 | 57.7 | 4 | 3 | US-09-039-308A-15 | Sequence 15, Appl |
| 30 | 15 | 57.7 | 4 | 3 | US-09-039-308A-17 | Sequence 17, Appl |
| 31 | 15 | 57.7 | 4 | 3 | US-09-270-735-2 | Sequence 2, Appl |
| 32 | 15 | 57.7 | 4 | 3 | US-09-167-921-42 | Sequence 42, Appl |
| 33 | 15 | 57.7 | 4 | 3 | US-09-270-736-1 | Sequence 1, Appl |
| 34 | 15 | 57.7 | 4 | 3 | US-08-973-462-29 | Sequence 29, Appl |
| 35 | 15 | 57.7 | 4 | 3 | US-08-761-483-3 | Sequence 3, Appl |
| 36 | 15 | 57.7 | 4 | 3 | US-08-761-483-10 | Sequence 10, Appl |
| 37 | 15 | 57.7 | 4 | 3 | US-09-323-743-42 | Sequence 42, Appl |
| 38 | 15 | 57.7 | 4 | 3 | US-09-058-969-2 | Sequence 2, Appl |
| 39 | 15 | 57.7 | 4 | 3 | US-09-130-193-1 | Sequence 1, Appl |
| 40 | 15 | 57.7 | 4 | 3 | US-09-130-193-7 | Sequence 7, Appl |
| 41 | 15 | 57.7 | 4 | 3 | US-09-130-193-12 | Sequence 12, Appl |
| 42 | 15 | 57.7 | 4 | 3 | US-09-130-193-15 | Sequence 15, Appl |
| 43 | 15 | 57.7 | 4 | 3 | US-09-357-952-5 | Sequence 5, Appl |
| 44 | 15 | 57.7 | 4 | 3 | US-09-309-003-1 | Sequence 1, Appl |
| 45 | 15 | 57.7 | 4 | 3 | US/08/869 | Sequence 1, Appl |

ALIGNMENTS

RESULT 1
US-10-015-328-8
; Sequence 8, Application US/10015328
; Patent No. 6727366
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; APPLICANT: Han, Amy Qi
; APPLICANT: Glunz, Peter W.
; TITLE OF INVENTION: Imidazolidinones and Their Related Derivatives as Hepatitis C VIR
; FILE REFERENCE: PH-7203
; CURRENT APPLICATION NUMBER: US/10/015,328
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255,168
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.
; NAME/KEY: MOD RES
; LOCATION: (1)-(1)
; OTHER INFORMATION: N-terminal Protecting Group: t-Butoxycarbonyl
; OTHER INFORMATION: Delta-Carboxy Ester: t-Butyl
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (2)-(2)
; OTHER INFORMATION: Gamma-Carboxy Ester: t-Butyl
; US-10-015-328-8
Query Match 100.0%; Score 26; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DEVP 5
DB 1 DEVP 5
RESULT 2
US-09-728-653-8
; Sequence 8, Application US/09728653
; Patent No. 6774212
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; APPLICANT: Han, Amy Qi

APPLICANT: Glunz, Peter W.
TITLE OF INVENTION: Alpha-Ketoamide Inhibitors of Hepatitis C Virus NS3 Protease
FILE REFERENCE: PH-7118
CURRENT APPLICATION NUMBER: US/09/728,653
CURRENT FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: US 60/168,998
PRIOR FILING DATE: 1999-12-03
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.
NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: N-terminal Protecting Group: t-Butoxycarbonyl
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (2)..(2)
OTHER INFORMATION: Delta-Carboxy Ester: t-Butyl
US-09-728-653-8

Query Match 100.0%; Score 26; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5
Db 1 DEVP 5

RESULT 3
US-10-015-328-9
Sequence 9, Application US/10015328
Patent No. 6727366
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
APPLICANT: Han, Amy Qi
APPLICANT: Glunz, Peter W.
TITLE OF INVENTION: Imidazolidinones and Their Related Derivatives as Hepatitis C Virus
FILE REFERENCE: PH-7203
CURRENT APPLICATION NUMBER: US/10/015,328
CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 60/255,168
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.
NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: N-terminal Protecting Group: benzyloxycarbonyl
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (4)..(4)
OTHER INFORMATION: Gamma-Carboxy Ester: t-Butyl
US-10-015-328-9

Query Match 76.9%; Score 20; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EVVP 5
Db 1 EVVP 4

RESULT 4
US-10-015-328-10
Sequence 10, Application US/10015328
Patent No. 6727366
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
APPLICANT: Han, Amy Qi
APPLICANT: Glunz, Peter W.
TITLE OF INVENTION: Imidazolidinones and Their Related Derivatives as Hepatitis C Virus
FILE REFERENCE: PH-7203
CURRENT APPLICATION NUMBER: US/10/015,328
CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 60/255,168
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.
NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: Gamma-Carboxy Ester: t-Butyl
US-10-015-328-10

Query Match 76.9%; Score 20; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EVVP 5
Db 1 EVVP 4

RESULT 5
US-09-728-653-9
Sequence 9, Application US/09728653
Patent No. 6774212
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
APPLICANT: Han, Amy Qi
APPLICANT: Glunz, Peter W.
TITLE OF INVENTION: Alpha-Ketoamide Inhibitors of Hepatitis C Virus NS3 Protease
FILE REFERENCE: PH-7118
CURRENT APPLICATION NUMBER: US/09/728,653
CURRENT FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: US 60/168,998
PRIOR FILING DATE: 1999-12-03
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.
NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: N-terminal Protecting Group: benzyloxycarbonyl
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (4)..(4)

OTHER INFORMATION: Benzyl Esterification
US-09-728-653-9

Query Match 76.9%; Score 20; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EVVP 5
Db 1 EVVP 4

RESULT 6
US-09-728-653-10
Sequence 10, Application US/09728653
Patent No. 6774212

GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
APPLICANT: Han, Amy Qi
APPLICANT: Glunz, Peter W.
TITLE OF INVENTION: Alpha-Ketamide Inhibitors of Hepatitis C Virus NS3 Protease
FILE REFERENCE: PH-7118
CURRENT APPLICATION NUMBER: US/09/728,653
CURRENT FILING DATE: 2000-12-01
PRIOR FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: US 60/168,998
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.
FEATURE:
NAME/KEY: MOD RES
LOCATION: (1)-(1)
OTHER INFORMATION: Gamma-Carboxy Ester: t-Butyl
US-09-728-653-10

Query Match 76.9%; Score 20; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EVVP 5
Db 1 EVVP 4

RESULT 7
US-09-020-880-41
Sequence 41, Application US/09020880A
Patent No. 6136558
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ballinger, Marcus D.
APPLICANT: Jones, Jennifer T.
APPLICANT: Fairbrother, Wayne J.
APPLICANT: Sliwowski, Mark X.
APPLICANT: Wells, James A.
TITLE OF INVENTION: HEPREGULIN VARIANTS
FILE REFERENCE: 14918-720CON1
CURRENT APPLICATION NUMBER: US/09/020,880A
CURRENT FILING DATE: 1998-02-09
EARLIER APPLICATION NUMBER: US 60/037,581
PRIOR FILING DATE: 1997-02-10
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 41
LENGTH: 5
TYPE: PRT
ORGANISM: No. 6136558 relevant (recombinant)
US-09-020-880-41

Query Match 65.4%; Score 17; DB 3; Length 5;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 EVVP 5
Db 2 EVVP 5

RESULT 8
US-09-101-544-41
Sequence 41, Application US/09101544
Patent No. 6387638

GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ballinger, Marcus D.
APPLICANT: Jones, Jennifer T.
APPLICANT: Fairbrother, Wayne J.
APPLICANT: Sliwowski, Mark X.
APPLICANT: Wells, James A.
TITLE OF INVENTION: HEPREGULIN VARIANTS
FILE REFERENCE: 14918-720CON2
CURRENT APPLICATION NUMBER: US/09/101,544
CURRENT FILING DATE: 1998-07-17
PRIOR APPLICATION NUMBER: US 09/020,880
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: US 60/037,581
PRIOR FILING DATE: 1997-02-10
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 41
LENGTH: 5
TYPE: PRT
ORGANISM: No. 6387638 relevant (recombinant)
US-09-101-544-41

Query Match 65.4%; Score 17; DB 3; Length 5;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 EVVP 5
Db 2 EVVP 5

RESULT 9
US-08-335-198-21
Sequence 21, Application US/08335198
Patent No. 5637454
GENERAL INFORMATION:
APPLICANT: Harley, John B.
TITLE OF INVENTION: Assays and Treatments for Autoimmune
NUMBER OF INVENTION: Diseases
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Kilpatrick & Cody
STREET: 1100 Peachtree Street, Ste. 2800
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30309-4539
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/335,198
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/648205

FILING DATE: 01-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF 114C1P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 815-6508
TRIEFAX: (404) 815-6555
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-335-198-21

Query Match 61.5%; Score 16; DB 1; Length 4;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 4
DB 1 DEVP 4

RESULT 10
US-09-357-952-68
Sequence 68, Application US/09357952
Patent No. 6248904
GENERAL INFORMATION:
APPLICANT: Zhang, Han-Zhong
APPLICANT: Cai, Sui Xiong
APPLICANT: Drewe, John A.
TITLE OF INVENTION: No. 6248904e1 Fluorescence Dyes and Their Applications for Whole-Cell Fluorescence Screening Assays for Caspases, Peptidases, Proteases
FILE REFERENCE: 1735.0030001
CURRENT FILING DATE: 1999-07-21
EARLIER APPLICATION NUMBER: US 60/093,642
EARLIER FILING DATE: 21-JUL-1998
NUMBER OF SEQ ID NOS: 139
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 68
LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-357-952-68

Query Match 61.5%; Score 16; DB 3; Length 5;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 EYVP 5
DB 1 DIVP 4

RESULT 11
US-09-521-650-68
Sequence 68, Application US/09521650
Patent No. 6335429
GENERAL INFORMATION:
APPLICANT: Weber, Eckard
APPLICANT: Keana, John F.W.
APPLICANT: Drewe, John A.
TITLE OF INVENTION: No. 6335429e1 Fluorescent Reporter Molecules and Their Applications for Whole-Cell Fluorescence Screening Assays for Caspases and Other Enzymes and the Use Thereof
FILE REFERENCE: 1735.0290002
CURRENT FILING DATE: 2000-03-08
EARLIER APPLICATION NUMBER: 09/168,888
EARLIER FILING DATE: 1998-10-09
EARLIER APPLICATION NUMBER: US 60/061,582
EARLIER FILING DATE: 1997-10-10
EARLIER APPLICATION NUMBER: US 09/033,661
EARLIER FILING DATE: 1998-03-03
NUMBER OF SEQ ID NOS: 142
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 68
LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-168-888-68

APPLICANT: Weber, Eckard
APPLICANT: Cai, Sui Xiong
APPLICANT: Keana, John F.W.
APPLICANT: Drewe, John A.
TITLE OF INVENTION: No. 6335429e1 Fluorescent Reporter Molecules and Their Applications for Whole-Cell Fluorescence Screening Assays for Caspases and Other Enzymes and the Use Thereof
FILE REFERENCE: 1735.0290002
CURRENT FILING DATE: 2000-03-08
EARLIER APPLICATION NUMBER: 09/168,888
EARLIER FILING DATE: 1998-10-09
EARLIER APPLICATION NUMBER: US 60/061,582
EARLIER FILING DATE: 1997-10-10
EARLIER APPLICATION NUMBER: US 09/033,661
EARLIER FILING DATE: 1998-03-03
NUMBER OF SEQ ID NOS: 142
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 68
LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-521-650-68

Query Match 61.5%; Score 16; DB 3; Length 5;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 EYVP 5
DB 1 DIVP 4

RESULT 12
US-09-168-888-68
Sequence 68, Application US/09168888
Patent No. 6342611
GENERAL INFORMATION:
APPLICANT: Weber, Eckard
APPLICANT: Cai, Sui Xiong
APPLICANT: Keana, John F.W.
TITLE OF INVENTION: No. 6342611e1 Fluorescent Reporter Molecules and Their Applications for Whole-Cell Fluorescence Screening Assays for Caspases and Other Enzymes and the Use Thereof
FILE REFERENCE: 1735.0290002
CURRENT FILING DATE: 1998-10-09
EARLIER APPLICATION NUMBER: US 60/061,582
EARLIER FILING DATE: 1997-10-10
EARLIER APPLICATION NUMBER: US 09/033,661
EARLIER FILING DATE: 1998-03-03
NUMBER OF SEQ ID NOS: 142
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 68
LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-168-888-68

Query Match 61.5%; Score 16; DB 3; Length 5;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 EVVP 5
: : :
Db 1 DIVP 4

RESULT 13
US-09-947-387-68
; Sequence 68, Application US/09947387
; Patent No. 6759207
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. 6759207el Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290005
; CURRENT APPLICATION NUMBER: US/09/947.387
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/061,582
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: US 60/145,746
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: US 09/168,888
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 68
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; US-09-947-387-68

Query Match 61.5%; Score 16; DB 4; Length 5;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 EVVP 5
: : :
Db 1 DIVP 4

RESULT 14
US-09-368-670C-10
; Sequence 10, Application US/09368670C
; Patent No. 6767991
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim (Canada) Ltd.
; TITLE OF INVENTION: Hepatitis C Inhibitor Peptides
; FILE REFERENCE: 13/063-2-C2
; CURRENT APPLICATION NUMBER: US/09/368.670C
; CURRENT FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,945
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/055,186
; PRIOR FILING DATE: 1997-08-11
; PRIOR APPLICATION NUMBER: 09/131,758
; PRIOR FILING DATE: 1998-08-10
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Hepatitis C
; FEATURE:
; NAME/KEY: VARIANT

; LOCATION: 1
; OTHER INFORMATION: Asp is capped with DAD
; US-09-368-670C-10
Query Match 61.5%; Score 16; DB 4; Length 5;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 EVVP 5
: : :
Db 1 DIVP 4

RESULT 15
US-09-368-670C-34
; Sequence 34, Application US/09368670C
; Patent No. 6767991
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim (Canada) Ltd.
; TITLE OF INVENTION: Hepatitis C Inhibitor Peptides
; FILE REFERENCE: 13/063-2-C2
; CURRENT APPLICATION NUMBER: US/09/368.670C
; CURRENT FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,945
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/055,186
; PRIOR FILING DATE: 1997-08-11
; PRIOR APPLICATION NUMBER: 09/131,758
; PRIOR FILING DATE: 1998-08-10
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Hepatitis C
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 5
; OTHER INFORMATION: Xaa=Nva
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 1
; OTHER INFORMATION: Asp is capped with DAD
; US-09-368-670C-34

Query Match 61.5%; Score 16; DB 4; Length 5;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 EVVP 5
: : :
Db 1 DIVP 4

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OM protein - protein search, using sw model

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(without alignments)
2.096 Million cell updates/sec

Title: SEQ1
Sequence: 1 decomp 5

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Gapop 10.0, Gapext 0.5

Searched: 1585576 seqs, 357178320 residues

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Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

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- 2: /cgn2_6/prodata/1/pubppa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/prodata/1/pubppa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/prodata/1/pubppa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/prodata/1/pubppa/US07_NEW_PUB.pep:*
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- 15: /cgn2_6/prodata/1/pubppa/US10_PUBCOMB.pep:*
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- 18: /cgn2_6/prodata/1/pubppa/US60_NEW_PUB.pep:*
- 19: /cgn2_6/prodata/1/pubppa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 26 | 100.0 | 5 | US-09-728-653-8 | Sequence 8, Appli |
| 2 | 26 | 100.0 | 5 | US-10-015-328-8 | Sequence 8, Appli |
| 3 | 20 | 76.9 | 4 | US-09-728-653-9 | Sequence 9, Appli |
| 4 | 20 | 76.9 | 4 | US-09-728-653-10 | Sequence 10, Appli |
| 5 | 20 | 76.9 | 4 | US-10-015-328-9 | Sequence 9, Appli |
| 6 | 20 | 76.9 | 4 | US-10-015-328-10 | Sequence 10, Appli |
| 7 | 17 | 65.4 | 5 | US-10-082-747A-41 | Sequence 41, Appli |
| 8 | 16 | 61.5 | 5 | US-09-777-785-2 | Sequence 2, Appli |
| 9 | 16 | 61.5 | 5 | US-09-777-785-4 | Sequence 4, Appli |
| 10 | 16 | 61.5 | 5 | US-09-777-785-5 | Sequence 5, Appli |
| 11 | 16 | 61.5 | 5 | US-09-777-785-6 | Sequence 6, Appli |
| 12 | 16 | 61.5 | 5 | US-09-947-387-68 | Sequence 68, Appli |
| 13 | 16 | 61.5 | 5 | US-10-138-375-68 | Sequence 68, Appli |

| | | | | | | |
|----|----|------|---|----|-------------------|--------------------|
| 14 | 16 | 61.5 | 5 | 17 | US-10-829-381-68 | Sequence 68, Appli |
| 15 | 15 | 57.7 | 4 | 8 | US-08-865-579-81 | Sequence 81, Appli |
| 16 | 15 | 57.7 | 4 | 8 | US-08-865-579-82 | Sequence 82, Appli |
| 17 | 15 | 57.7 | 4 | 9 | US-09-045-620-4 | Sequence 4, Appli |
| 18 | 15 | 57.7 | 4 | 9 | US-09-734-846-42 | Sequence 42, Appli |
| 19 | 15 | 57.7 | 4 | 9 | US-09-746-731-81 | Sequence 81, Appli |
| 20 | 15 | 57.7 | 4 | 9 | US-09-746-731-82 | Sequence 82, Appli |
| 21 | 15 | 57.7 | 4 | 9 | US-09-799-463-2 | Sequence 2, Appli |
| 22 | 15 | 57.7 | 4 | 9 | US-09-735-363A-85 | Sequence 85, Appli |
| 23 | 15 | 57.7 | 4 | 9 | US-09-799-994-2 | Sequence 2, Appli |
| 24 | 15 | 57.7 | 4 | 9 | US-09-745-204-2 | Sequence 2, Appli |
| 25 | 15 | 57.7 | 4 | 9 | US-09-780-142-3 | Sequence 71, Appli |
| 26 | 15 | 57.7 | 4 | 9 | US-09-765-105-2 | Sequence 3, Appli |
| 27 | 15 | 57.7 | 4 | 9 | US-09-858-754-6 | Sequence 6, Appli |
| 28 | 15 | 57.7 | 4 | 9 | US-09-858-754-11 | Sequence 11, Appli |
| 29 | 15 | 57.7 | 4 | 9 | US-09-858-754-11 | Sequence 3, Appli |
| 30 | 15 | 57.7 | 4 | 9 | US-09-987-417-3 | Sequence 2, Appli |
| 31 | 15 | 57.7 | 4 | 9 | US-09-863-649-2 | Sequence 1, Appli |
| 32 | 15 | 57.7 | 4 | 9 | US-09-737-255-1 | Sequence 1, Appli |
| 33 | 15 | 57.7 | 4 | 9 | US-09-920-332-1 | Sequence 8, Appli |
| 34 | 15 | 57.7 | 4 | 9 | US-09-845-028-8 | Sequence 52, Appli |
| 35 | 15 | 57.7 | 4 | 9 | US-09-954-687-52 | Sequence 9, Appli |
| 36 | 15 | 57.7 | 4 | 9 | US-09-270-983-9 | Sequence 5, Appli |
| 37 | 15 | 57.7 | 4 | 9 | US-09-947-387-5 | Sequence 29, Appli |
| 38 | 15 | 57.7 | 4 | 9 | US-09-742-096-29 | Sequence 1, Appli |
| 39 | 15 | 57.7 | 4 | 10 | US-09-819-266-1 | Sequence 2, Appli |
| 40 | 15 | 57.7 | 4 | 10 | US-09-161-172-2 | Sequence 7, Appli |
| 41 | 15 | 57.7 | 4 | 10 | US-09-866-512A-7 | Sequence 1, Appli |
| 42 | 15 | 57.7 | 4 | 10 | US-09-862-224-1 | Sequence 6, Appli |
| 43 | 15 | 57.7 | 4 | 13 | US-10-103-448-6 | Sequence 3, Appli |
| 44 | 15 | 57.7 | 4 | 13 | US-10-099-408A-3 | Sequence 81, Appli |
| 45 | 15 | 57.7 | 4 | 13 | US-10-059-749-81 | Sequence 81, Appli |

ALIGNMENTS

RESULT 1
US-09-728-653-8
Sequence 8, Application US/09728653
Publication No. US20020123468A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
APPLICANT: Han, Amy Qi
APPLICANT: Glum, Peter W.
TITLE OF INVENTION: Alpha-Helcoamide Inhibitors of Hepatitis C Virus NS3 Protease
FILE REFERENCE: PH-7118
CURRENT APPLICATION NUMBER: US/09/728,653
CURRENT FILING DATE: 2000-12-01
PRIORITY FILING DATE: 1999-12-03
PRIORITY FILING DATE: 1999-12-03
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.
FEATURE:
NAME/KEY: MOD RES
LOCATION: (1)..(1)
OTHER INFORMATION: N-terminal Protecting Group: t-Butoxycarbonyl
OTHER INFORMATION: Delta-Carboxy Ester: t-Butyl
FEATURE:
NAME/KEY: MOD RES
LOCATION: (2)..(2)
OTHER INFORMATION: Gamma-Carboxy Ester: t-Butyl
US-09-728-653-8
Query Match 100.0%; Score 26; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5
Db 1 DEVP 5

RESULT 2

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US-10-015-328-8
; Sequence 8, Application US/10015328
; Publication No. US20030100768A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; APPLICANT: Han, Amy Qi
; APPLICANT: Glunz, Peter W.
; TITLE OF INVENTION: Imidazolidinones and Their Related Derivatives as Hepatitis C Virus
; FILE REFERENCE: PH-7203
; CURRENT APPLICATION NUMBER: US/10/015,328
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255,168
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.
; NAME/KEY: MOD RES
; LOCATION: (1)-(1)
; OTHER INFORMATION: N-terminal Protecting Group: t-Butoxycarbonyl
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (2)-(2)
; OTHER INFORMATION: Delta-Carboxy Ester: t-Butyl
US-10-015-328-8
; OTHER INFORMATION: Gamma-Carboxy Ester: t-Butyl

```

Query Match 100.0%; Score 26; DB 14; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5
Db 1 DEVP 5

RESULT 3

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US-09-728-653-9
; Sequence 9, Application US/09728653
; Publication No. US20020123468A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; APPLICANT: Han, Amy Qi
; APPLICANT: Glunz, Peter W.
; TITLE OF INVENTION: Alpha-Ketamide Inhibitors of Hepatitis C Virus NS3 Protease
; FILE REFERENCE: PH-7118
; CURRENT APPLICATION NUMBER: US/09/728,653
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 60/168,998
; PRIOR FILING DATE: 1999-12-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.
; NAME/KEY: MOD_RES

```

```

; LOCATION: (1)..(1)
; OTHER INFORMATION: N-terminal Protecting Group: benzyloxycarbonyl
; OTHER INFORMATION: Gamma-Carboxy Ester: t-Butyl
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (4)-(4)
; OTHER INFORMATION: Benzyl Esterification
US-09-728-653-9

```

Query Match 76.9%; Score 20; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EYVP 5
Db 1 EYVP 4

RESULT 4

```

US-09-728-653-10
; Sequence 10, Application US/09728653
; Publication No. US20020123468A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; APPLICANT: Han, Amy Qi
; APPLICANT: Glunz, Peter W.
; TITLE OF INVENTION: Alpha-Ketamide Inhibitors of Hepatitis C Virus NS3 Protease
; FILE REFERENCE: PH-7118
; CURRENT APPLICATION NUMBER: US/09/728,653
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 60/168,998
; PRIOR FILING DATE: 1999-12-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.
; NAME/KEY: MOD RES
; LOCATION: (1)-(1)
; OTHER INFORMATION: Gamma-Carboxy Ester: t-Butyl
US-09-728-653-10

```

Query Match 76.9%; Score 20; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EYVP 5
Db 1 EYVP 4

RESULT 5

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US-10-015-328-9
; Sequence 9, Application US/10015328
; Publication No. US20030100768A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; APPLICANT: Han, Amy Qi
; APPLICANT: Glunz, Peter W.
; TITLE OF INVENTION: Imidazolidinones and Their Related Derivatives as Hepatitis C Virus
; FILE REFERENCE: PH-7203
; CURRENT APPLICATION NUMBER: US/10/015,328
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255,168
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9

```

```

; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: N-terminal Protecting Group: benzylloxycarbonyl
; OTHER INFORMATION: Gamma-Carboxy Ester: t-Butyl
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: Benzyl Esterification
US-10-015-328-9
;
Query Match          76.9%; Score 20; DB 14; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY      2 EVVP 5
        |||
Db       1 EVVP 4

RESULT 6
US-10-015-328-10
; Sequence 10, Application US/10015328
; Publication No. US20030100768A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; APPLICANT: Han, Amy Q1
; APPLICANT: Glunz, Peter W.
; TITLE OF INVENTION: Imidazolidinones and Their Related Derivatives as Hepatitis C Vir
; TITLE OF INVENTION: Protease Inhibitors
; FILE REFERENCE: PH-7203
; CURRENT APPLICATION NUMBER: US/10/015,328
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255,168
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: Gamma-Carboxy Ester: t-Butyl
US-10-015-328-10
;
Query Match          76.9%; Score 20; DB 14; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY      2 EVVP 5
        |||
Db       1 EVVP 4

RESULT 7
US-10-082-747A-41
; Sequence 41, Application US/10082747A
; Publication No. US20030129688A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ballinger, Marcus D.
; APPLICANT: Jones, Jennifer T.
; APPLICANT: Fairbrother, Wayne J.
; APPLICANT: Slikowski, Mark X.
; APPLICANT: Slikowski, Mark X.
```

```

; APPLICANT: Wells, James A.
; TITLE OF INVENTION: HEREGULIN VARIANTS
; FILE REFERENCE: 402E-4/612US
; CURRENT APPLICATION NUMBER: US/10/082,747A
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/101,544
; PRIOR FILING DATE: 1998-07-17
; PRIOR APPLICATION NUMBER: PCT/US/98/01579
; PRIOR FILING DATE: 1998-02-10
; PRIOR APPLICATION NUMBER: US 08/799,054
; PRIOR FILING DATE: 1997-02-10
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatsEQ for Windows Version 3.0
; SEQ ID NO 41
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence at human heregulin-beta1
; OTHER INFORMATION: residues 177-181
US-10-082-747A-41
;
Query Match          65.4%; Score 17; DB 14; Length 5;
Best Local Similarity 75.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
;
QY      2 EVVP 5
        |||
Db       2 EVVP 5

RESULT 8
US-09-777-785-2
; Sequence 2, Application US/09777785
; Patent No. US20020103135A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Ruzhin
; TITLE OF INVENTION: Azapeptides Useful In The Treatment Of Hepatitis C
; FILE REFERENCE: IN01130K1 US
; CURRENT APPLICATION NUMBER: US/09/777,785
; CURRENT FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/181,017
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:azapeptide
; NAME/KEY: MOD RES
; LOCATION: (1)
; OTHER INFORMATION: ACETYLATION
; NAME/KEY: UNSURE
; LOCATION: (5)
; OTHER INFORMATION: 2-[(4-nitrophenoxy)carbonyl]-2-propylhydrazine
; NAME/KEY: UNSURE
; LOCATION: (2)
; OTHER INFORMATION: Xaa=D-gamma-carboxyglutamic acid
US-09-777-785-2
;
Query Match          61.5%; Score 16; DB 9; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
;
QY      1 DEVP 5
        |||
Db       1 EVVP 5

RESULT 9
US-09-777-785-4
```

```
/ Sequence 4, Application US/09777785
/ Patent No. US20020103135A1
/ GENERAL INFORMATION:
/ APPLICANT: Zhang, Rumin
/ TITLE OF INVENTION: Azapeptides Useful In The Treatment Of Hepatitis C
/ FILE REFERENCE: IN01130X1 US
/ CURRENT APPLICATION NUMBER: US/09/777,785
/ PRIOR FILING DATE: 2001-02-06
/ PRIOR APPLICATION NUMBER: 60/181,017
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 4
/ LENGTH: 5
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:azapeptide
/ NAME/KEY: MOD_RES
/ LOCATION: (1)
/ OTHER INFORMATION: ACETYLATION
/ NAME/KEY: UNSURE
/ LOCATION: (5)
/ OTHER INFORMATION: 2-[(1-chloro-2-methylpropyloxy)carbonyl]-2-propylhy
/ OTHER INFORMATION: ydrazine
/ NAME/KEY: UNSURE
/ LOCATION: (2)
/ OTHER INFORMATION: Xaa=D-gamma-carboxyglutamic acid
US-09-777-785-4
```

```
Query Match      61.5%; Score 16; DB 9; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 DEVP 5
       : |||
Db      1 EXVVP 5
```

```
RESULT 10
US-09-777-785-5
/ Sequence 5, Application US/09777785
/ Patent No. US20020103135A1
/ GENERAL INFORMATION:
/ APPLICANT: Zhang, Rumin
/ TITLE OF INVENTION: Azapeptides Useful In The Treatment Of Hepatitis C
/ FILE REFERENCE: IN01130X1 US
/ CURRENT APPLICATION NUMBER: US/09/777,785
/ PRIOR FILING DATE: 2001-02-06
/ PRIOR APPLICATION NUMBER: 60/181,017
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 5
/ LENGTH: 5
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:azapeptide
/ NAME/KEY: MOD_RES
/ LOCATION: (1)
/ OTHER INFORMATION: ACETYLATION
/ NAME/KEY: UNSURE
/ LOCATION: (5)
/ OTHER INFORMATION: 2-[(chloromethoxy)carbonyl]-2-propylhydrazine
/ NAME/KEY: UNSURE
/ LOCATION: (2)
/ OTHER INFORMATION: Xaa=D-gamma-carboxyglutamic acid
US-09-777-785-5
```

```
Query Match      61.5%; Score 16; DB 9; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 DEVP 5
       : |||
Db      1 EXVVP 5
```

```
RESULT 11
US-09-777-785-6
/ Sequence 6, Application US/09777785
/ Patent No. US20020103135A1
/ GENERAL INFORMATION:
/ APPLICANT: Zhang, Rumin
/ TITLE OF INVENTION: Azapeptides Useful In The Treatment Of Hepatitis C
/ FILE REFERENCE: IN01130X1 US
/ CURRENT APPLICATION NUMBER: US/09/777,785
/ PRIOR FILING DATE: 2001-02-06
/ PRIOR APPLICATION NUMBER: 60/181,017
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 6
/ LENGTH: 5
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:azapeptide
/ NAME/KEY: MOD_RES
/ LOCATION: (1)
/ OTHER INFORMATION: ACETYLATION
/ NAME/KEY: UNSURE
/ LOCATION: (5)
/ OTHER INFORMATION: 2-[(1,2,2,2-tetrachloroethoxy)carbonyl]-2-propylhy
/ OTHER INFORMATION: drazine
/ NAME/KEY: UNSURE
/ LOCATION: (2)
/ OTHER INFORMATION: Xaa=D-gamma-carboxyglutamic acid
US-09-777-785-6
```

```
Query Match      61.5%; Score 16; DB 9; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 DEVP 5
       : |||
Db      1 EXVVP 5
```

```
RESULT 12
US-09-947-387-68
/ Sequence 68, Application US/09947387
/ Patent No. US20020150885A1
/ GENERAL INFORMATION:
/ APPLICANT: Weber, Eckard
/ APPLICANT: Cai, Sui Xiong
/ APPLICANT: Keane, John F.W.
/ APPLICANT: Drewe, John A.
/ APPLICANT: Zhang, Han-Zhong
/ TITLE OF INVENTION: No. US20020150885A1el Fluorogenic or Fluorescent Reporter Molecule
/ TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
/ TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
/ FILE REFERENCE: 1735.0290005
/ CURRENT APPLICATION NUMBER: US/09/947,387
/ PRIOR FILING DATE: 2001-09-07
/ PRIOR APPLICATION NUMBER: US 60/061,582
/ PRIOR FILING DATE: 1997-10-10
/ PRIOR APPLICATION NUMBER: US 60/145,746
/ PRIOR FILING DATE: 1998-03-03
/ PRIOR APPLICATION NUMBER: US 09/168,888
/ NUMBER OF SEQ ID NOS: 142
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 68
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LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Peptide
US-09-947-387-68

Query Match 61.5%; Score 16; DB 9; Length 5;
Best Local Similarity 50.0%; Pred. No. 1.4e+06;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 EVVP 5
Db 1 DIVP 4

RESULT 13
US-10-138-375-68
Sequence 68, Application US/10138375
Publication No. US20030208037A1
GENERAL INFORMATION:
APPLICANT: Zhang, Han-Zhong
APPLICANT: Cai, Sui Xiong
APPLICANT: Drewe, John A.
APPLICANT: Yang, Wu
TITLE OF INVENTION: No. US20030208037A1 Fluorescence Dyes and Their Applications for
TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Protease
TITLE OF INVENTION: Other Enzymes and the Use Thereof
FILE REFERENCE: 1735-0030001
CURRENT APPLICATION NUMBER: US/10/138,375
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/357,952
PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-21
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/093,642
PRIOR FILING DATE: EARLIER FILING DATE: 21-JUL-1998
NUMBER OF SEQ ID NOS: 139
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 68
LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Peptide
US-10-138-375-68

Query Match 61.5%; Score 16; DB 14; Length 5;
Best Local Similarity 50.0%; Pred. No. 1.4e+06;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 EVVP 5
Db 1 DIVP 4

RESULT 14
US-10-829-381-68
Sequence 68, Application US/10829381
Publication No. US20040191844A1
GENERAL INFORMATION:
APPLICANT: Weber, Eckard
APPLICANT: Cai, Sui Xiong
APPLICANT: Keana, John F.W.
APPLICANT: Drewe, John A.
APPLICANT: Zhang, Han-Zhong
TITLE OF INVENTION: Novel Fluorogenic or Fluorescent Reporter Molecules and
TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
TITLE OF INVENTION: Use Thereof
FILE REFERENCE: 1735-0290006
CURRENT APPLICATION NUMBER: US/10/829,381
CURRENT FILING DATE: 2004-04-22

PRIOR APPLICATION NUMBER: US 60/061,582
PRIOR FILING DATE: 1997-10-10
PRIOR APPLICATION NUMBER: US 60/145,746
PRIOR FILING DATE: 1998-03-03
PRIOR APPLICATION NUMBER: US 09/168,888
PRIOR FILING DATE: 1998-10-09
PRIOR APPLICATION NUMBER: US 09/947,387
PRIOR FILING DATE: 2001-09-07
NUMBER OF SEQ ID NOS: 142
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 68
LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Peptide
US-10-829-381-68

Query Match 61.5%; Score 16; DB 17; Length 5;
Best Local Similarity 50.0%; Pred. No. 1.4e+06;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 EVVP 5
Db 1 DIVP 4

RESULT 15
US-08-865-579-81
Sequence 81, Application US/08865579
Publication No. US20010006779A1
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandes-Alnemri, Teresa
APPLICANT: Litwack, Gerald
TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
TITLE OF INVENTION: Encoding Same and Methods of Use
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
City: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/865,579
FILING DATE: 29-MAY-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 2180
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-9849
INFORMATION FOR SEQ ID NO: 81:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 4
OTHER INFORMATION: /note="Amino Acid is bonded to an
OTHER INFORMATION: aldehyde at the C-terminal."

US-08-865-579-81

Query Match

Best Local Similarity 57.7%; Score 15; DB 8; Length 4;

Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 1 DEV 3

Db 1 DEV 3

Search completed: December 8, 2004, 08:48:38
Job time : 853 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 8, 2004, 08:30:15 ; Search time 38 Seconds
(without alignments)
12.660 Million cell updates/sec

Title: SEQ1
Perfect score: 26
Sequence: 1 devp 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 206

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | * Match Length | DB ID | Description |
|------------|-------|-------------------|-------|---------------------------|
| 1 | 46.2 | 4 | 2 | A61300 22K superhelical D |
| 2 | 42.3 | 4 | 2 | Schwannomin - mous |
| 3 | 42.3 | 4 | 2 | ribosomal protein |
| 4 | 42.3 | 5 | 2 | R-phycocerythrin al |
| 5 | 42.3 | 5 | 2 | Ig heavy chain CRD |
| 6 | 42.3 | 5 | 2 | T-cell receptor be |
| 7 | 42.3 | 5 | 2 | T-cell receptor be |
| 8 | 42.3 | 5 | 2 | glycogen phosphory |
| 9 | 42.3 | 5 | 2 | trkA protein - Bsc |
| 10 | 34.6 | 5 | 2 | fulicin - giant Af |
| 11 | 30.8 | 3 | 3 | tyrosine protein k |
| 12 | 30.8 | 3 | 3 | bioerin A - Clitroba |
| 13 | 30.8 | 5 | 1 | peptidyl-dipeptida |
| 14 | 30.8 | 5 | 2 | hypocretinal prote |
| 15 | 30.8 | 5 | 2 | T-cell receptor de |
| 16 | 30.8 | 5 | 2 | flagellar protein |
| 17 | 30.8 | 5 | 2 | proctolin - Atlant |
| 18 | 30.8 | 5 | 2 | T-cell receptor be |
| 19 | 30.8 | 5 | 3 | thryoliberin - she |
| 20 | 26.9 | 3 | 3 | thryoliberin - eas |
| 21 | 26.9 | 3 | 3 | thryoliberin - Bom |
| 22 | 26.9 | 3 | 3 | TPH-like tripeptid |
| 23 | 26.9 | 3 | 3 | thryoliberin - pig |
| 24 | 26.9 | 3 | 3 | phagocytosis-stimu |
| 25 | 26.9 | 4 | 2 | scarvation-induced |
| 26 | 26.9 | 4 | 2 | glucan 1,4-alpha-g |
| 27 | 26.9 | 4 | 2 | RPCH-related neuro |
| 28 | 26.9 | 4 | 2 | |
| 29 | 26.9 | 4 | 2 | |

| | | | | | | |
|----|---|------|---|---|--------|--------------------|
| 30 | 7 | 26.9 | 4 | 2 | 151049 | metallothionein-A |
| 31 | 7 | 26.9 | 4 | 2 | PT0240 | Ig heavy chain CRD |
| 32 | 7 | 26.9 | 4 | 2 | S55238 | pallidipin - assas |
| 33 | 7 | 26.9 | 4 | 2 | PI0140 | carbon-monoxide de |
| 34 | 7 | 26.9 | 4 | 2 | PT0271 | Ig heavy chain CRD |
| 35 | 7 | 26.9 | 4 | 2 | PT0675 | T-cell receptor be |
| 36 | 7 | 26.9 | 4 | 2 | A32039 | tyrosine-melanocyl |
| 37 | 7 | 26.9 | 5 | 2 | UN0862 | peptidyl-dipeptida |
| 38 | 7 | 26.9 | 5 | 2 | C41225 | copper resistance |
| 39 | 7 | 26.9 | 5 | 2 | A41225 | copper resistance |
| 40 | 7 | 26.9 | 5 | 2 | B60274 | major protein anti |
| 41 | 7 | 26.9 | 5 | 2 | E60274 | major protein anti |
| 42 | 7 | 26.9 | 5 | 2 | P00009 | angiotensin-conver |
| 43 | 7 | 26.9 | 5 | 2 | P00689 | photosystem I 10.4 |
| 44 | 7 | 26.9 | 5 | 2 | PS0324 | ribulose-bisphosph |
| 45 | 7 | 26.9 | 5 | 2 | B37988 | acid proteinase 11 |

ALIGNMENTS

RESULT 1
A61300
22K superhelical DNA-binding protein - Escherichia coli (fragment)
C:Species: Escherichia coli
C:Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 07-May-1999
C:Accession: A61300
R:Kishi, F.; Ebina, Y.; Miyai, T.; Nakazawa, T.; Nakazawa, A.
J. Biochem. 92, 1059-1068, 1982
A:Title: Purification and characterization of a protein from Escherichia coli which forms
A:Reference number: A61300; MUID:83082696; PMID:6294066
A:Accession: A61300
A:Molecule type: protein
A:Residues: 1-4 <KIS>
A:Comment: This protein resembles some of the histone-like protein of bacteria in amino
C:Keywords: DNA binding; monomer

Query Match 46.2% Score 12; DB 2; Length 4;
Best Local Similarity 66.7% Pred. No. 2.8e+05; Indels 0; Gaps 0;
Matches 2; Conservative 1; Mismatches 0;

QY 2 EVV 4
DB 2 EIV 4

RESULT 2
I54357
Schwannomin - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C:Accession: I54357
R:Huyh, D.P.; Nechiporuk, T.; Puls, S.
Hum. Mol. Genet. 3, 1075-1079, 1994
A:Title: Alternative transcripts in the mouse neurofibromatosis type 2 (NF2) gene are co
A:Reference number: I54357; MUID:95072570; PMID:7981675
A:Accession: I54357
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-4 <RFS>
A:Cross-references: GB:I28038; NID:G454836; PIDN:AAA57150.1; PID:G601923
C:Genetics:
A:Gene: NF2

Query Match 42.3% Score 11; DB 2; Length 4;
Best Local Similarity 100.0% Pred. No. 2.8e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY 4 VP 5
DB 1 VP 2

RESULT 3
S17255
ribosomal protein Yml1, mitochondrial, questionable - Yeast (Saccharomyces cerevisiae)
C/Species: Saccharomyces cerevisiae
A/Variety: strain 07173
C/Date: 23-Apr-1993 #sequence_revision 14-Sep-1994 #text_change 09-Jul-2004
C/Accession: S17255
R/Grohmann, L.; Graak, H.R.; Kruff, V.; Choli, T.; Goldschmidt-Reisin, S.; Kitakawa, M.
A/Title: Extended N-terminal sequencing of proteins of the large ribosomal subunit from
A/Reference number: S17255; PMID:91265106; PMID:2060626
A/Accession: S17255
A/Molecule type: protein
A/Residues: 1-4 <GRO>
A/Cross-references: UNIPROT:P36515
C/Comment: A coding region for this protein could not be identified in the genome of Sac
C/Genetics:
A/Genome: nuclear
C/Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 42.3%; Score 11; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVP 5
DB 2 VVP 4

RESULT 4
B22565
R-phycocerythrin alpha-2 chain - red alga (Gastrocionium coulteri) (fragment)
C/Species: Gastrocionium coulteri
C/Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C/Accession: B22565
R/Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A/Title: Characterization of the bilin attachment sites in R-phycocerythrin.
A/Reference number: A22565; PMID:85182601; PMID:3886644
A/Accession: B22565
A/Molecule type: protein
A/Residues: 1-5 <KLO>

Query Match 42.3%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VP 5
DB 3 VP 4

RESULT 5
PT0281
Ig heavy chain CRD3 region (clone 4-91C) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C/Accession: PT0281
R/Yamada, M.; Waserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A/Reference number: PT0222; PMID:91108337; PMID:1899102
A/Accession: PT0281
A/Molecule type: DNA
A/Residues: 1-5 <YAM>
A/Experimental source: B lymphocyte
C/Keywords: heterotetramer; immunoglobulin

Query Match 42.3%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DE 2

DB 1 DE 2

RESULT 6
PT0656
T-cell receptor beta chain V-D-J region (121-107) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C/Accession: PT0656
R/Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A/Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A/Reference number: PT0509; PMID:91277601; PMID:1711558
A/Accession: PT0656
A/Status: translation not shown
A/Molecule type: mRNA
A/Residues: 1-5 <FEE>
A/Experimental source: day 4 postnatal thymus, strain BALB/c
C/Keywords: T-cell receptor

Query Match 42.3%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DE 2
DB 4 DE 5

RESULT 7
PT0573
T-cell receptor beta chain V-D-J region (141-100) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C/Accession: PT0573
R/Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A/Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A/Reference number: PT0509; PMID:91277601; PMID:1711558
A/Accession: PT0573
A/Status: translation not shown
A/Molecule type: mRNA
A/Residues: 1-5 <FEE>
A/Experimental source: day 19 fetal thymus, strain BALB/c
C/Keywords: T-cell receptor

Query Match 42.3%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DE 2
DB 4 DE 5

RESULT 8
A60521
glycogen phosphorylase (BC 2.4.1.1), muscle - mullet (Liza ramada) (fragment)
N/Alternate names: glycogen phosphorylase b
C/Species: Liza ramada
C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 15-Mar-2004
C/Accession: A60521
R/Bonamura, L.; Baanante, I.V.
Comp. Biochem. Physiol. B 95, 295-301, 1990
A/Title: Purification and characterization of glycogen phosphorylase B from skeletal musc
A/Reference number: A60521; PMID:90227907; PMID:2109669
A/Accession: A60521
A/Molecule type: protein
A/Residues: 1-5 <BON>
C/Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein
F3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experime

Query Match 42.3%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VP 5
DB 4 VP 5

RESULT 9

A32014
tram protein - Escherichia coli plasmid R100 (fragment)
C:Species: Escherichia coli
C:Date: 22-Jun-1989 #sequence_revision 22-Jun-1989 #text_change 09-Jul-2004
C:Accession: A32014
R:Inamoto, S.; Yoshioaka, Y.; Ohtsubo, E.
J. Bacteriol. 170, 2749-2757, 1988
A:Title: Identification and characterization of the products from the traA and traY genes
A:Reference number: A32014; MUID:88227859; PMID:2836369
A:Accession: A32014
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-5 <DNA>
A:Cross-references: UNIPROT:P13973
C:Genetics:
A:Genome: plasmid
C:Keywords: DNA binding

Query Match 42.3%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DE 2
DB 3 DE 4

RESULT 10

A44692
fulicin - giant African snail
C:Species: Achatina fulica (giant African snail)
C:Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
C:Accession: A44692
R:Ohba, N.; Kubota, I.; Takeo, T.; Shimomishi, Y.; Yaeuda-Kamatani, Y.; Minakata, H.; No
Biochem. Biophys. Res. Commun. 178, 486-493, 1991
A:Title: Fulicin, a novel neuropeptide containing a D-amino acid residue isolated from t
A:Reference number: A44692; MUID:91315471; PMID:1859408
A:Accession: A44692
A:Molecule type: protein
A:Residues: 1-5 <OH>
A:Cross-references: UNIPROT:P35905
C:Keywords: amidated carboxyl end; D-amino acid; neuropeptide
F:2/Modified site: D-asparagine (Asn) #status experimental
F:5/Modified site: amidated carboxyl end (Val) #status experimental

Query Match 34.6%; Score 9; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEVV 4
DB 2 NEVV 5

RESULT 11

I78890
tyrosine protein kinase - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C:Accession: I78890
R:Chow, L.W.; Davidson, D.; Fournel, M.; Gosselin, P.; Lemieux, S.; Lyu, M.S.; Kozak, C.
Oncogene 9, 3437-3448, 1994
A:Title: Two distinct protein isoforms are encoded by ntK, a csk-related tyrosine protei

A:Reference number: I58407; MUID:95060800; PMID:7970703

A:Accession: I78890
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-3 <RES>
A:Cross-references: GB:I33339; NID:G609536; PID:AAA64432.1; PID:G609538
C:Genetics:
A:Gene: p52nk

Query Match 30.8%; Score 8; DB 3; Length 3;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 VP 5
DB 1 MP 2

RESULT 12

I10697
biotin A - Citrobacter freundii (fragment)
C:Species: Citrobacter freundii
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C:Accession: I10697
R:Shuan, D.; Campbell, A.
Gene 67, 203-211, 1988
A:Title: Transcriptional regulation and gene arrangement of Escherichia coli, Citrobacter
A:Reference number: I10697; MUID:89006280; PMID:2971595
A:Accession: I10697
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-4 <RES>
A:Cross-references: UNIPROT:P13071; GB:M21922; NID:G144434

Query Match 30.8%; Score 8; DB 2; Length 4;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DE 2
DB 3 DD 4

RESULT 13

H080HA
proctolin - American cockroach
C:Species: Periplaneta americana (American cockroach)
C:Date: 29-Jul-1981 #sequence_revision 29-Jul-1981 #text_change 09-Jul-2004
C:Accession: A01644
R:Staratt, A.N.; Brown, B.E.
Life Sci. 17, 1253-1256, 1975
A:Title: Structure of the pentapeptide proctolin, a proposed neurotransmitter in insect
A:Reference number: A93048; MUID:76074708; PMID:576
A:Accession: A01644
A:Molecule type: protein
A:Residues: 1-5 <STA>
A:Cross-references: UNIPROT:P01373
A:Note: The synthetic peptide had the same chromatographic, electrophoretic, and pharma
R:O'Shea, M.; Adams, M.E.
Science 213, 567-569, 1981
A:Title: Pentapeptide (proctolin) associated with an identified neuron.
A:Reference number: A94260; MUID:81225865; PMID:6113690
A:Contents: annotation; biological source
C:Comment: This peptide is found in the lateral white neurons, which occur (in the cock
innervate the striated hindgut muscles in insects and stimulate contraction of these m
C:Superfamily: proctolin
C:Keywords: neuropeptide

Query Match 30.8%; Score 8; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 VP 5

Db :|
3 LP 4

RESULT 14

JN0860
peptidyl-dipeptidase A inhibitory peptide C107 - striped bonito
C:Species: Sarda orientalis (striped bonito)
C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999
C:Accession: JN0860
R:Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.
Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993
A:Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory pe
A:Reference number: JN0859; MUID:94080036; PMID:7764272
A:Molecule type: Protein
A:Residues: 1-5 <MAT>
A:Experimental source: Intestine
C:Comment: The carboxyl-terminus is essential for the protein's expression of angiotensin
C:Superfamily: bradykinin-potentiating peptide
C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 30.8%; Score 8; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 VP 5
:|
Db 2 LP 3

RESULT 15

S53595
hypothetical protein (upstream of transcription factor, CCAAT-binding) - chicken
C:Species: Gallus gallus (chicken)
C:Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 07-May-1999
C:Accession: S53595
R:Galkhoven, C.F.; Bouwman, P.R.J.; Snippe, L.; Ab, G.
Nucleic Acids Res. 22, 5540-5547, 1994
A:Title: Translational start site multiplicity of the CCAAT/enhancer binding protein alpha
A:Reference number: S53595; MUID:5510613; PMID:7838705
A:Accession: S53595
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-5 <CAL>
A:Cross-references: EMBL:X66844

Query Match 30.8%; Score 8; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 VP 5
:|
Db 1 MP 2

Search completed: December 8, 2004, 08:31:02
Job time : 40 secs

GenCore version 5.1.6
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OW protein - protein search, using sw model

Run on: December 8, 2004, 08:33:45 ; Search time 62 Seconds
(without alignments)
46.401 Million cell updates/sec

Title: SEQ1
Perfect score: 26
Sequence: 1 devvp 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Uniprot_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|----------------------|
| 1 | 26 | 100.0 | 42 | 027873 | 027873 methanobact |
| 2 | 26 | 100.0 | 56 | 02742T2 | 02742T2 mycobacteri |
| 3 | 26 | 100.0 | 56 | AA803070 | AA803070 mycobacte |
| 4 | 26 | 100.0 | 74 | Q9XUG8 | Q9XUG8 caenorhabdi |
| 5 | 26 | 100.0 | 77 | Q8SEPX3 | Q8SEPX3 canis fami |
| 6 | 26 | 100.0 | 87 | Q77X97 | Q77X97 helicoverpa |
| 7 | 26 | 100.0 | 87 | Q77M48 | Q77M48 helicoverpa |
| 8 | 26 | 100.0 | 87 | Q99H26 | Q99H26 helicoverpa |
| 9 | 26 | 100.0 | 87 | Q8Y5W7 | Q8Y5W7 helicoverpa |
| 10 | 26 | 100.0 | 90 | Q7R242 | Q7R242 cryza sativ |
| 11 | 26 | 100.0 | 90 | BAC98628 | BAC98628 cryza sat |
| 12 | 26 | 100.0 | 99 | Q8EN67 | Q8EN67 caenorhabdi |
| 13 | 26 | 100.0 | 100 | Q6GB20 | Q6GB20 staphylococ |
| 14 | 26 | 100.0 | 100 | Q6GJH3 | Q6GJH3 staphylococ |
| 15 | 26 | 100.0 | 100 | Q8NXZ8 | Q8NXZ8 staphylococ |
| 16 | 26 | 100.0 | 102 | Q49991 | Q49991 lycopersico |
| 17 | 26 | 100.0 | 108 | Q99W45 | Q99W45 staphylococ |
| 18 | 26 | 100.0 | 108 | Q7A785 | Q7A785 staphylococ |
| 19 | 26 | 100.0 | 111 | Q8HXV3 | Q8HXV3 sagittinus os |
| 20 | 26 | 100.0 | 111 | Q8HXV4 | Q8HXV4 macaca sp. |
| 21 | 26 | 100.0 | 111 | Q8HXV5 | Q8HXV5 pongo pygma |
| 22 | 26 | 100.0 | 111 | Q8HXV6 | Q8HXV6 gorilla gor |
| 23 | 26 | 100.0 | 111 | Q8HXV7 | Q8HXV7 pan troglod |
| 24 | 26 | 100.0 | 115 | Q21175 | Q21175 caenorhabdi |
| 25 | 26 | 100.0 | 120 | Q32933 | Q32933 mycobacteri |
| 26 | 26 | 100.0 | 129 | Q9CBT7 | Q9CBT7 mycobacteri |
| 27 | 26 | 100.0 | 150 | Q93T65 | Q93T65 bruceella su |
| 28 | 26 | 100.0 | 150 | Q8FT05 | Q8FT05 bruceella su |
| 29 | 26 | 100.0 | 150 | Q92M97 | Q92M97 rhizobium m |
| 30 | 26 | 100.0 | 150 | Q8FTV3 | Q8FTV3 bruceella me |
| 31 | 26 | 100.0 | 152 | Q8FTW99 | Q8FTW99 bruceella su |

| | | | | | | |
|----|----|-------|-----|---|------------|------------------------|
| 32 | 26 | 100.0 | 152 | 2 | 08YC25 | 08YC25 bruceella me |
| 33 | 26 | 100.0 | 153 | 1 | ANF_FELCA | ANF_FELCA felis silve |
| 34 | 26 | 100.0 | 153 | 1 | ANF_HUMAN | ANF_HUMAN homo sapien |
| 35 | 26 | 100.0 | 153 | 2 | Q6TFY3 | Q6TFY3 erwinia amy |
| 36 | 26 | 100.0 | 153 | 2 | AAQ97887 | AAQ97887 erwinia a |
| 37 | 26 | 100.0 | 155 | 2 | Q9RIG1 | Q9RIG1 rattus norv |
| 38 | 26 | 100.0 | 161 | 2 | Q6LCX4 | Q6LCX4 sus scrofa |
| 39 | 26 | 100.0 | 161 | 2 | Q982Z1 | Q982Z1 rhizobium 1 |
| 40 | 26 | 100.0 | 161 | 2 | AA60467 | AA60467 sus scrof |
| 41 | 26 | 100.0 | 169 | 2 | Q6CPA6 | Q6CPA6 apis mellif |
| 42 | 26 | 100.0 | 169 | 2 | AA820468 | AA820468 apis mell |
| 43 | 26 | 100.0 | 170 | 1 | SPRT_YERPE | SPRT_YERPE yersinia pe |
| 44 | 26 | 100.0 | 170 | 2 | Q6D080 | Q6D080 erwinia car |
| 45 | 26 | 100.0 | 176 | 2 | Q930U3 | Q930U3 rhizobium m |

ALIGNMENTS

RESULT 1

ID 027873 PRELIMINARY; PRT; 42 AA.
AC 027873;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Hypothetical protein MTH1845.
GN OrderedLocustNames=MTH1845;
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=187420;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Delta H;
RA MEDLINE=98037514; PubMed=9371463;
RA Smith D.R., Doncette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
RA Aldredge T., Bashirzadeh R., Blakey D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McDougall S., Shiner G., Goyal A., Pietrowski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
deltaH: functional analysis and comparative genomics.";
RL J. Bacteriol. 179:7135-7155(1997).
DR EMBL; AE000937; AAB86311.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 42 AA; 4806 MW; E60FC64EAL53E91 CRC64;

Query Match 100.0%; Score 26; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2

ID 0742T2 PRELIMINARY; PRT; 66 AA.
AC 0742T2;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=MAP0753c;
OS Mycobacterium paratuberculosis.
OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium;
OC Mycobacterium avium complex (MAC).

OK NCBI_TaxID=1770;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K10;
 RA Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapur V.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AE017229; AAS03070.1; -
 DR InterPro: IPR001080; 3Fe4SFeDOXin.
 DR PRINTS: PR00352; 3FE4SFeDOXin.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 66 AA; 7199 MW; F691DE3C4BE6F393 CRC64;

Query Match 100.0%; Score 26; DB 2; Length 66;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5
 Db 37 DEVP 41

RESULT 3
 AAS03070 PRELIMINARY; PRT; 66 AA.
 ID AAS03070;
 AC AAS03070;
 DT 02-MAR-2004 (TREMBlrel. 27, Created)
 DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
 DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
 DE Hypothetical protein.
 GN MAP0753C.
 OS Mycobacterium paratuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1770;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K10;
 RA Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapur V.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AE017229; AAS03070.1; -
 DR Hypothetical protein.
 KW SEQUENCE 66 AA; 7199 MW; F691DE3C4BE6F393 CRC64;
 SQ SEQUENCE 66 AA; 7199 MW; F691DE3C4BE6F393 CRC64;
 Query Match 100.0%; Score 26; DB 2; Length 66;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DEVP 5
 Db 37 DEVP 41

RESULT 4
 Q9XUG8 PRELIMINARY; PRT; 74 AA.
 ID Q9XUG8;
 AC Q9XUG8;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Hypothetical protein C43F9.7.
 GN Name=C43F9.7;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C. elegans: A platform for
 RL Science 282:2012-2018 (1998).

RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Bristol N2;
 RA Mortimore B.J.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: Z82262; CAB05150.1; -
 DR PIR: T19911; T19911
 DR WormRep: C43F9.7; CE19735.
 KW Hypothetical protein.
 SQ SEQUENCE 74 AA; 8436 MW; 1437C36FALB4E9F4 CRC64;

Query Match 100.0%; Score 26; DB 2; Length 74;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5
 Db 30 DEVP 34

RESULT 5
 Q8SPX3 PRELIMINARY; PRT; 77 AA.
 ID Q8SPX3;
 AC Q8SPX3;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Atrial natriuretic peptide (Fragment).
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RA Rastogi S., Tiwari N., Mishra S., Sabbah H.N., Gupta R.C.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF484116; AAL92021.1; -
 DR CO: GO:0005576; Cxcracellular; IEA.
 DR CO: GO:0005179; Fihormone activity; IEA.
 DR CO: GO:0007582; Pihysiological process; IEA.
 DR InterPro: IPR002407; Ac_natriurecep.
 DR InterPro: IPR000663; Natr_peptide.
 DR Pfam: PF00212; ANP; 1.
 DR PRINTS: PR00711; ANATPEPTIDE.
 FT NON TER 1
 FT NON TER 77
 SQ SEQUENCE 77 AA; 8290 MW; 32D36091AB7D752 CRC64;
 Query Match 100.0%; Score 26; DB 2; Length 77;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5
 Db 22 DEVP 26

RESULT 6
 Q77K97 PRELIMINARY; PRT; 87 AA.
 ID Q77K97;
 AC Q77K97;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE P10.
 OS Helicoverpa armigera nuclear polyhedrosis virus.
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 OC Nucleopolyhedrovirus.
 OX NCBI_TaxID=51313;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang C.X., Wu J.C.;


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RT "Genome structure and the p10 gene of the Helicoverpa armigera
  nucleopolyhedrovirus.";
RL Acta Biochim. Biophys. Sin. 33:179-184(2001).
DR EMBL: AF303045; AAK36274.1; -.
DR InterPro: IPR008702; NPV_P10.
DR Pfam: PF05531; NPV_P10; 1.
SQ SEQUENCE 87 AA; 9331 MW; 30A98644B22293FA CRC64;

Query Match
Best Local Similarity 100.0%; Score 26; DB 2; Length 87;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5
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Db 73 DEVP 77

RESULT 7
Q77M48 PRELIMINARY; PRT; 87 AA.
AC Q77M48;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE p10.
OS Helicoverpa armigera single nucleocapsid polyhedrovirus.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
CX NCBI_TaxID=160266;
RN [1]
RP SEQUENCE FROM N.A.
RA Wang H., Chen X., Viak J.M., Hu Z.;
RT "Sequence and transcriptional analysis of the p10 gene of Helicoverpa
  armigera single nucleocapsid polyhedrovirus.";
RL Ping Tu Hsueh Pac 17:81-86(2001).
DR EMBL: AF265354; AAK57874.1; -.
DR InterPro: IPR008702; NPV_P10.
DR Pfam: PF05531; NPV_P10; 1.
SQ SEQUENCE 87 AA; 9331 MW; 30A98644B22293FA CRC64;

Query Match
Best Local Similarity 100.0%; Score 26; DB 2; Length 87;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5
   |||||
Db 73 DEVP 77

RESULT 8
Q99H26 PRELIMINARY; PRT; 87 AA.
ID Q99H26;
AC Q99H26;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE p10.
OS Helicoverpa armigera nucleopolyhedrovirus G4.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
CX NCBI_TaxID=148363;
RN [1]
RP SEQUENCE FROM N.A.
RA Deng F., Chen X., Viak J.M., Arif B.M., Hu Z.;
RT "Sequence analysis of the gp37 gene of Heliothis armigera single-
  nucleocapsid nucleopolyhedrovirus.";
RL Zhongguo Bing Du Xue 15:35-42(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Wang H., Hu Z., Sun X., Viak J.M., Chen X.;
RT "Sequence analysis of the gp37 gene of Heliothis armigera single-
  nucleocapsid nucleopolyhedrovirus.";
RL Zhongguo Bing Du Xue 15:43-49(2000).

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RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21078302; PubMed=11210934;
RA Wang H., Chen X., Wang H., Arif B.M., Viak J.M., Hu Z.;
RT "Nucleotide sequence and transcriptional analysis of a putative basic
  DNA-binding protein of Helicoverpa armigera polyhedrovirus.";
RL Virus Genes 22:113-120(2001).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=21064569; PubMed=1125177;
RA Chen X., Ickel W.F., Tarchini R., Sun X., Sandbrink H., Wang H.,
  Peters S., Zuidema D., Iankhorst R.K., Viak J.M., Hu Z.;
RT "The sequence of the Helicoverpa armigera single-nucleocapsid
  nucleopolyhedrovirus genome.";
RL J. Gen. Virol. 82:241-257(2001).
DR EMBL: AF271059; AAG53764.1; -.
DR GO: GO:0019028; C:viral capsid; IEA.
DR InterPro: IPR008702; NPV_P10.
DR Pfam: PF05531; NPV_P10; 1.
SQ SEQUENCE 87 AA; 9331 MW; 30A98644B22293FA CRC64;

Query Match
Best Local Similarity 100.0%; Score 26; DB 2; Length 87;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5
   |||||
Db 73 DEVP 77

RESULT 9
Q8V5W7 PRELIMINARY; PRT; 87 AA.
ID Q8V5W7;
AC Q8V5W7;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE ORF20.
OS Helicoverpa zea single nucleocapsid nucleopolyhedrovirus.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
CX NCBI_TaxID=10468;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21830929; PubMed=11842262;
RA Chen X., Zhang W.-J., Wong J., Chun G., Lu A., McCutchen B.F.,
  Presnail J.K., Herrmann R., Dolan M., Tingey S., Hu Z.-H., Viak J.M.;
RT "Comparative analysis of the complete genome sequences of Helicoverpa
  zea and Helicoverpa armigera single-nucleocapsid
  nucleopolyhedroviruses.";
RL J. Gen. Virol. 83:673-684(2002).
DR EMBL: AF34030; AAD56165.1; -.
DR GO: GO:0019028; C:viral capsid; IEA.
DR InterPro: IPR008702; NPV_P10.
DR Pfam: PF05531; NPV_P10; 1.
SQ SEQUENCE 87 AA; 9353 MW; 30A98A48B22B9FFA CRC64;

Query Match
Best Local Similarity 100.0%; Score 26; DB 2; Length 87;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5
   |||||
Db 73 DEVP 77

RESULT 10
Q7E242 PRELIMINARY; PRT; 90 AA.
ID Q7E242;
AC Q7E242;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)

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DE Hypochemical protein B101SH11.112.
 GN Name=B101SH11.112;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 RN NCB1_TaxID=39947;
 RP SEQUENCE FROM N.A.
 RA Sasaki T., Matsumoto T., Katayose Y.,
 RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP005123; BAC98628.1; -.
 KW Hypochemical protein.
 SQ SEQUENCE 90 AA; 9784 MW; F76FADCA9444E184 CRC64;

Query Match 100.0%; Score 26; DB 2; Length 90;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DEVP 5
 DB 85 DEVP 89

RESULT 11
 ID BAC98628 PRELIMINARY; PRT; 90 AA.
 AC BAC98628;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DE Hypochemical protein B101SH11.112.
 GN B101SH11.112.
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza; Oryza sativa.
 RN NCB1_TaxID=39947;
 RP SEQUENCE FROM N.A.
 RA Sasaki T., Matsumoto T., Katayose Y.,
 RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP005123; BAC98628.1; -.
 KW Hypochemical protein.
 SQ SEQUENCE 90 AA; 9784 MW; F76FADCA9444E184 CRC64;

Query Match 100.0%; Score 26; DB 2; Length 90;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DEVP 5
 DB 85 DEVP 89

RESULT 12
 ID Q86NG7 PRELIMINARY; PRT; 99 AA.
 AC Q86NG7;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypochemical protein K03B4.7.
 GN Name=K03B4.7;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 RN NCB1_TaxID=6239;
 RP SEQUENCE FROM N.A.

RC STRAIN-Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA Wilson R.;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Du Z., Le T.T., Kemp K.;
 RL Submitted (Apr-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Wilson R.;
 RL Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U55370; AA021423.1; -.
 KW Hypochemical protein.
 SQ SEQUENCE 99 AA; 11281 MW; AEFCCCB4E8527A5 CRC64;

Query Match 100.0%; Score 26; DB 2; Length 99;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DEVP 5
 DB 22 DEVP 26

RESULT 13
 ID Q6GBZ0 PRELIMINARY; PRT; 100 AA.
 AC Q6GBZ0;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Stage V sporulation protein G.
 GN ORFNames=SA50455;
 OS Staphylococcus aureus subsp. aureus MSSA476.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 RN NCB1_TaxID=282459;
 RP SEQUENCE FROM N.A.
 RC STRAIN=MSSA476;
 RA Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barton A.,
 RA Baason N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
 RA Fellwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
 RA James K.D., Lennard N., Line A., Mayes R., Mould S., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrall B.G.,
 RA Spratt B.G., Parkhill J.;
 RT "Complete genomes of two clinical Staphylococcus aureus strains:
 RT evidence for the rapid evolution of virulence and drug resistance.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 DR EMBL; BX571857; CAG42230.1; -.
 DR InterPro; IPR007170; SpovG.
 DR Pfam; PF04026; SpovG; 1.
 SQ SEQUENCE 100 AA; 11278 MW; 876EC2BC87CF74C CRC64;

Query Match 100.0%; Score 26; DB 2; Length 100;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DEVP 5
 DB 84 DEVP 88

RESULT 14

OG6GH3 PRELIMINARY; PRT; 100 AA.
 AC OG6GH3;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 GN Stage V sporulation protein G.
 OS Name=spovG; ORFNames=SA0499;
 OC Staphylococcus aureus subsp. aureus MRSA252.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=282458;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MRSA252;
 RA Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
 RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
 RA Feltwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
 RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
 RA Spratt B.G., Parkhill J.;
 RT "Complete genomes of two clinical Staphylococcus aureus strains:
 RT evidence for the rapid evolution of virulence and drug resistance.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791 (2004).
 DR EMBL; BX571856; CAG39521.1; -;
 DR InterPro; IPR007170; SpovG.
 DR Pfam; PF04026; SpovG; 1.
 SQ SEQUENCE 100 AA; 11290 MW; 87B189C87CF7F4C CRC64;

Query Match

Best Local Similarity 100.0%; Score 26; DB 2; Length 100;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5
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DB 84 DEVP 88

RESULT 15

OGNXZ8 PRELIMINARY; PRT; 100 AA.
 AC OGNXZ8;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 GN SpovG protein.
 OS Name=spovG; OrderedLocustNames=M0453;
 OC Staphylococcus aureus (strain MW2).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=196620;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MW2;
 RA MEDLINE=22040717; PubMed=12044378;
 RA Baba T., Takeuchi F., Kuroda M., Aoki K.-I., Oguuchi A.,
 RA Nagai Y., Iwama N., Asano K., Naito T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiramoto K.;
 RT "Genome and virulence determinants of high virulence community-
 RT acquired MRSA.";
 RL Lancet 359:1819-1827 (2002).
 DR EMBL; AP004823; BAB94318.1; -;
 DR GO; GO:0030435; P:sporulation; IEA.
 DR InterPro; IPR007170; SpovG.
 DR Pfam; PF04026; SpovG; 1.
 KW Complete proteome.
 SQ SEQUENCE 100 AA; 11278 MW; 87EC2BC87CF7F4C CRC64;

Query Match

100.0%; Score 26; DB 2; Length 100;

Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5
 |||||

DB 84 DEVP 88

Search completed: December 8, 2004, 08:55:47
 Job time : 65 secs

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OM protein - protein search, using sw model

Run on: December 8, 2004, 08:48:48 ; Search time 37 Seconds

(without alignments)
8.962 Million cell updates/sec

Title: SEQ1
Perfect score: 26
Sequence: 1 devvp 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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4: /cgn2_6/prodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/iaa/PCUTUS_COMB.pep:*
6: /cgn2_6/prodata/1/iaa/backfileseq1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|---------------------|
| 1 | 26 | 100.0 | 5 | 4 | US-10-015-328-8 |
| 2 | 26 | 100.0 | 5 | 4 | US-09-728-653-8 |
| 3 | 26 | 100.0 | 6 | 4 | US-10-015-328-5 |
| 4 | 26 | 100.0 | 6 | 4 | US-10-015-328-7 |
| 5 | 26 | 100.0 | 6 | 4 | US-10-015-328-11 |
| 6 | 26 | 100.0 | 6 | 4 | US-09-728-653-5 |
| 7 | 26 | 100.0 | 6 | 4 | US-09-728-653-7 |
| 8 | 26 | 100.0 | 6 | 4 | US-09-728-653-11 |
| 9 | 26 | 100.0 | 125 | 2 | US-08-862-480B-1 |
| 10 | 26 | 100.0 | 135 | 4 | US-09-270-767-35928 |
| 11 | 26 | 100.0 | 135 | 4 | US-09-270-767-35928 |
| 12 | 26 | 100.0 | 135 | 4 | US-09-270-767-35928 |
| 13 | 26 | 100.0 | 135 | 4 | US-09-270-767-35928 |
| 14 | 26 | 100.0 | 151 | 3 | US-08-916-043-5 |
| 15 | 26 | 100.0 | 151 | 3 | US-08-916-043-5 |
| 16 | 26 | 100.0 | 151 | 3 | US-08-916-043-5 |
| 17 | 26 | 100.0 | 151 | 3 | US-08-916-043-5 |
| 18 | 26 | 100.0 | 151 | 3 | US-08-916-043-5 |
| 19 | 26 | 100.0 | 151 | 3 | US-08-916-043-5 |
| 20 | 26 | 100.0 | 151 | 3 | US-08-916-043-5 |
| 21 | 26 | 100.0 | 151 | 3 | US-08-916-043-5 |
| 22 | 26 | 100.0 | 151 | 3 | US-08-916-043-5 |
| 23 | 26 | 100.0 | 151 | 3 | US-08-916-043-5 |
| 24 | 26 | 100.0 | 151 | 3 | US-08-916-043-5 |
| 25 | 26 | 100.0 | 151 | 3 | US-08-916-043-5 |
| 26 | 26 | 100.0 | 151 | 3 | US-08-916-043-5 |
| 27 | 26 | 100.0 | 151 | 3 | US-08-916-043-5 |

| | | | | | | |
|----|----|-------|------|---|----------------------|-------------------|
| 28 | 26 | 100.0 | 538 | 4 | US-09-248-796A-20842 | Sequence 20842, A |
| 29 | 26 | 100.0 | 715 | 4 | US-09-489-039A-12511 | Sequence 12511, A |
| 30 | 26 | 100.0 | 998 | 4 | US-08-252-991A-24402 | Sequence 24402, A |
| 31 | 26 | 100.0 | 1171 | 4 | US-09-489-039A-10298 | Sequence 10298, A |
| 32 | 26 | 100.0 | 1189 | 4 | US-09-489-039A-13776 | Sequence 13776, A |
| 33 | 26 | 96.2 | 6 | 4 | US-09-368-670C-11 | Sequence 11, Appl |
| 34 | 26 | 96.2 | 18 | 3 | US-08-522-269B-9 | Sequence 9, Appl |
| 35 | 26 | 96.2 | 18 | 3 | US-08-522-269B-9 | Sequence 9, Appl |
| 36 | 26 | 96.2 | 65 | 4 | US-08-248-796A-21591 | Sequence 21591, A |
| 37 | 26 | 96.2 | 110 | 3 | US-09-134-001C-3334 | Sequence 3334, Ap |
| 38 | 26 | 96.2 | 121 | 2 | US-08-576-626A-51 | Sequence 51, Appl |
| 39 | 26 | 96.2 | 149 | 4 | US-09-735-846-4 | Sequence 4, Appl |
| 40 | 26 | 96.2 | 150 | 4 | US-09-735-846-4 | Sequence 4, Appl |
| 41 | 26 | 96.2 | 186 | 4 | US-09-248-796A-19755 | Sequence 19755, A |
| 42 | 26 | 96.2 | 194 | 4 | US-09-735-846-6 | Sequence 6, Appl |
| 43 | 26 | 96.2 | 226 | 4 | US-09-555-510B-12 | Sequence 12, Appl |
| 44 | 26 | 96.2 | 226 | 4 | US-10-231-013-12 | Sequence 12, Appl |
| 45 | 26 | 96.2 | 264 | 4 | US-09-602-787A-98 | Sequence 98, Appl |

ALIGNMENTS

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RESULT 1
US-10-015-328-8
; Sequence 8, Application US/10015328
; Patent No. 6727366
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; APPLICANT: Han, Amy Qi
; APPLICANT: Glunz, Peter W.
; TITLE OF INVENTION: Imidazolidinones and Their Related Derivatives as Hepatitis C Virus
; TITLE OF INVENTION: Protease Inhibitors
; FILE REFERENCE: PH-7203
; CURRENT APPLICATION NUMBER: US/10/015,328
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255,168
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: N-terminal Protecting Group: t-Butoxycarbonyl
; FEATURE:
; OTHER INFORMATION: Delta-Carboxy Ester: t-Butyl
; NAME/KEY: MOD RES
; LOCATION: (2)..(2)
; OTHER INFORMATION: Gamma-Carboxy Ester: t-Butyl
US-10-015-328-8

Query Match          100.0%  Score 26;  DB 4;  Length 5;
Best Local Similarity 100.0%  Pred. No. 3.8e+05;
Matches 5;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY 1 DEVVP 5
DB 1 DEVVP 5

RESULT 2
US-09-728-653-8
; Sequence 8, Application US/09728653
; Patent No. 6774212
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; APPLICANT: Han, Amy Qi
```

```
APPLICANT: Glunz, Peter W.
TITLE OF INVENTION: Alpha-ketamide Inhibitors of Hepatitis C Virus NS3 Protease
FILE REFERENCE: PH-7118
CURRENT APPLICATION NUMBER: US/09/728,653
CURRENT FILING DATE: 2000-12-01
PRIORITY APPLICATION NUMBER: US 60/168,998
PRIOR FILING DATE: 1999-12-03
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: N-terminal Protecting Group: t-Butoxycarbonyl
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (2)..(2)
OTHER INFORMATION: Delta-Carboxy Ester: t-Butyl
OTHER INFORMATION: Gamma-Carboxy Ester: t-Butyl
US-09-728-653-8
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Query Match      100.0%; Score 26; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 DEVP 5
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Db      1 DEVP 5
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RESULT 3
US-10-015-328-5
Sequence 5, Application US/10015328
Patent No. 6727366
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
APPLICANT: Han, Amy Qi
APPLICANT: Glunz, Peter W.
TITLE OF INVENTION: Imidazolidinones and Their Related Derivatives as Hepatitis C Virus
FILE REFERENCE: PH-7203
CURRENT APPLICATION NUMBER: US/10/015,328
CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 60/255,168
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6)..(6)
OTHER INFORMATION: Boro-allylglycine
US-10-015-328-5
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Query Match      100.0%; Score 26; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 DEVP 5
      |||||
Db      1 DEVP 5
```

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RESULT 4
US-10-015-328-7
Sequence 7, Application US/10015328
Patent No. 6727366
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
APPLICANT: Han, Amy Qi
APPLICANT: Glunz, Peter W.
TITLE OF INVENTION: Imidazolidinones and Their Related Derivatives as Hepatitis C Virus
FILE REFERENCE: PH-7203
CURRENT APPLICATION NUMBER: US/10/015,328
CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 60/255,168
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6)..(6)
OTHER INFORMATION: Boro-allylglycine pinanediol ester
US-10-015-328-7
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Query Match      100.0%; Score 26; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 DEVP 5
      |||||
Db      1 DEVP 5
```

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RESULT 5
US-10-015-328-11
Sequence 11, Application US/10015328
Patent No. 6727366
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
APPLICANT: Han, Amy Qi
APPLICANT: Glunz, Peter W.
TITLE OF INVENTION: Imidazolidinones and Their Related Derivatives as Hepatitis C Virus
FILE REFERENCE: PH-7203
CURRENT APPLICATION NUMBER: US/10/015,328
CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 60/255,168
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: N-terminal Protecting Group: t-Butoxycarbonyl
OTHER INFORMATION: Delta-Carboxy Ester: t-Butyl
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (2)..(2)
OTHER INFORMATION: Gamma-Carboxy Ester: t-Butyl
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6)..(6)
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; OTHER INFORMATION: Boro-allylglycine pinanediol ester
; US-10-015-328-11
Query Match
Best Local Similarity 100.0%; Score 26; DB 4; Length 6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVP 5
Db 1 DEVP 5

RESULT 6
US-09-728-653-5
; Sequence 5, Application US/09728653
; Patent No. 6774212
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; APPLICANT: Han, Amy Qi
; APPLICANT: Glunz, Peter W.
; TITLE OF INVENTION: Alpha-Ketoamide Inhibitors of Hepatitis C Virus NS3 Protease
; FILE REFERENCE: PH-7118
; CURRENT APPLICATION NUMBER: US/09/728,653
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 60/168,998
; PRIOR FILING DATE: 1999-12-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.
; NAME/KEY: MISC FEATURE
; LOCATION: (6)..(6)
; OTHER INFORMATION: Boro-allylglycine
US-09-728-653-5

Query Match
Best Local Similarity 100.0%; Score 26; DB 4; Length 6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVP 5
Db 1 DEVP 5

RESULT 7
US-09-728-653-7
; Sequence 7, Application US/09728653
; Patent No. 6774212
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; APPLICANT: Han, Amy Qi
; APPLICANT: Glunz, Peter W.
; TITLE OF INVENTION: Alpha-Ketoamide Inhibitors of Hepatitis C Virus NS3 Protease
; FILE REFERENCE: PH-7118
; CURRENT APPLICATION NUMBER: US/09/728,653
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 60/168,998
; PRIOR FILING DATE: 1999-12-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.
; NAME/KEY: MISC FEATURE
; LOCATION: (6)..(6)
; OTHER INFORMATION: Boro-allylglycine
US-09-728-653-7

Query Match
Best Local Similarity 100.0%; Score 26; DB 4; Length 6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVP 5
Db 1 DEVP 5

RESULT 8
US-09-728-653-11
; Sequence 11, Application US/09728653
; Patent No. 6774212
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; APPLICANT: Han, Amy Qi
; APPLICANT: Glunz, Peter W.
; TITLE OF INVENTION: Alpha-Ketoamide Inhibitors of Hepatitis C Virus NS3 Protease
; FILE REFERENCE: PH-7118
; CURRENT APPLICATION NUMBER: US/09/728,653
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 60/168,998
; PRIOR FILING DATE: 1999-12-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: N-terminal Protecting Group: t-Butoxycarbonyl
; FEATURE:
; OTHER INFORMATION: Delta-Carboxy Ester: t-Buyl
; NAME/KEY: MOD RES
; LOCATION: (2)..(2)
; OTHER INFORMATION: Gamma-Carboxy Ester: t-Buyl
; NAME/KEY: MISC FEATURE
; LOCATION: (6)..(6)
; OTHER INFORMATION: Boro-allylglycine pinanediol ester
US-09-728-653-11

Query Match
Best Local Similarity 100.0%; Score 26; DB 4; Length 6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVP 5
Db 1 DEVP 5

RESULT 9
US-08-862-480B-1
; Sequence 1, Application US/08862480B
; Patent No. 5965533
; GENERAL INFORMATION:
; APPLICANT: Chen, Chi J.; Shockley, Ty R.; and
; APPLICANT: Johnston, Miles G.
; TITLE OF INVENTION: Atrial Natriuretic Peptide
; TITLE OF INVENTION: Peritoneal Dialysis Solutions
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESS: Thomas Borecki
; STREET: 1620 N. Waukegan Road
```

```
; LOCATION: (6)..(6)
; OTHER INFORMATION: Boro-allylglycine pinanediol ester
; US-09-728-653-7
Query Match
Best Local Similarity 100.0%; Score 26; DB 4; Length 6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVP 5
Db 1 DEVP 5

RESULT 8
US-09-728-653-11
; Sequence 11, Application US/09728653
; Patent No. 6774212
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; APPLICANT: Han, Amy Qi
; APPLICANT: Glunz, Peter W.
; TITLE OF INVENTION: Alpha-Ketoamide Inhibitors of Hepatitis C Virus NS3 Protease
; FILE REFERENCE: PH-7118
; CURRENT APPLICATION NUMBER: US/09/728,653
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 60/168,998
; PRIOR FILING DATE: 1999-12-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: N-terminal Protecting Group: t-Butoxycarbonyl
; FEATURE:
; OTHER INFORMATION: Delta-Carboxy Ester: t-Buyl
; NAME/KEY: MOD RES
; LOCATION: (2)..(2)
; OTHER INFORMATION: Gamma-Carboxy Ester: t-Buyl
; NAME/KEY: MISC FEATURE
; LOCATION: (6)..(6)
; OTHER INFORMATION: Boro-allylglycine pinanediol ester
US-09-728-653-11

Query Match
Best Local Similarity 100.0%; Score 26; DB 4; Length 6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVP 5
Db 1 DEVP 5

RESULT 9
US-08-862-480B-1
; Sequence 1, Application US/08862480B
; Patent No. 5965533
; GENERAL INFORMATION:
; APPLICANT: Chen, Chi J.; Shockley, Ty R.; and
; APPLICANT: Johnston, Miles G.
; TITLE OF INVENTION: Atrial Natriuretic Peptide
; TITLE OF INVENTION: Peritoneal Dialysis Solutions
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESS: Thomas Borecki
; STREET: 1620 N. Waukegan Road
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CITY: McGaw Park
STATE: Illinois
COUNTRY: USA
ZIP: 60085
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/862,480B
FILING DATE: 23-MAY-1997
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acid residues
TYPE: amino acid
STRANDEDNESS: No. 5965533 Relevant
TOPOLOGY: No. 5965533 Relevant
MOLECULE TYPE: peptide
US-08-862-480B-1

Query Match 100.0%; Score 26; DB 2; Length 125;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5
DB 30 DEVP 34

RESULT 10
US-09-270-767-39928
Sequence 39928, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 39928
LENGTH: 135
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-270-767-39928

Query Match 100.0%; Score 26; DB 4; Length 135;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5
DB 112 DEVP 116

RESULT 11
US-09-270-767-55145
Sequence 55145, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 55145
LENGTH: 135
TYPE: PRT

ORGANISM: Drosophila melanogaster
US-09-270-767-55145

Query Match 100.0%; Score 26; DB 4; Length 135;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5
DB 112 DEVP 116

RESULT 12
5212286-4
Patent No. 5212286
APPLICANT: LEWICKI, JOHN A.; SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR
PEPTIDE COMPOUNDS
NUMBER OF SEQUENCES: 68
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/870,795
FILING DATE: 05-JUN-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 766,030
FILING DATE: 08-MAY-1985
APPLICATION NUMBER: 602,117
FILING DATE: 09-APR-1984
APPLICATION NUMBER: 616,488
FILING DATE: 01-JUN-1984
SEQ ID NO: 4
LENGTH: 136
5212286-4

Query Match 100.0%; Score 26; DB 6; Length 136;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5
DB 40 DEVP 44

RESULT 13
US-08-916-043-5
Sequence 5, Application US/08916043
Patent No. 6013630
GENERAL INFORMATION:
APPLICANT: Shimkets, Richard A.
TITLE OF INVENTION: ATRIAL NATRIURETIC FACTOR MUTANTS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/916,043
FILING DATE: 21-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mastrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7934-048
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864

TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 151 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-916-043-5

Query Match 100.0%; Score 26; DB 3; Length 151;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVP 5
Db 55 DEVP 59

RESULT 14
US-09-428-929-5
Sequence 5, Application US/09428929
Patent No. 6514939
GENERAL INFORMATION:
APPLICANT: Shinkens, Richard A.
TITLE OF INVENTION: ATRIAL NATRIURETIC FACTOR MUTANTS
TITLE OF INVENTION: AND ISCHEMIC STROKE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/428,929
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/916,043
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7934-048
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 151 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-428-929-5

Query Match 100.0%; Score 26; DB 4; Length 151;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVP 5
Db 55 DEVP 59

RESULT 15

5212286-2
Patent No. 5212286
APPLICANT: LEWICKI, JOHN A.; SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR
PEPTIDE COMPOUNDS
NUMBER OF SEQUENCES: 68
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/870,795
FILING DATE: 05-JUN-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 766,030
FILING DATE: 08-MAY-1985
APPLICATION NUMBER: 602,117
FILING DATE: 09-APR-1984
APPLICATION NUMBER: 616,488
FILING DATE: 01-JUN-1984
SEQ ID NO: 2
LENGTH: 151

Query Match 100.0%; Score 26; DB 6; Length 151;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVP 5
Db 55 DEVP 59

Search completed: December 8, 2004, 08:57:13
Job time : 38 secs

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OM protein - protein search, using SW model

Run on: December 8, 2004, 08:52:01 ; Search time 143 Seconds

(without alignments)
12.489 Million cell updates/sec

Title: SEQ1

Perfect score: 26

Sequence: 1 decomp 5

Scoring table:

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Gapop 10.0, Gapext 0.5

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1585576

Total number of hits satisfying chosen parameters:

1585576

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Published Applications AA:*
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16: /cgn2_6/ptodata/1/pubppaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubppaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|----------------------|
| 1 | 26 | 100.0 | 5 | 9 | US-09-728-653-8 |
| 2 | 26 | 100.0 | 5 | 14 | US-10-015-328-8 |
| 3 | 26 | 100.0 | 6 | 9 | US-09-728-653-5 |
| 4 | 26 | 100.0 | 6 | 9 | US-09-728-653-7 |
| 5 | 26 | 100.0 | 6 | 9 | US-09-728-653-11 |
| 6 | 26 | 100.0 | 6 | 14 | US-10-010-184A-5 |
| 7 | 26 | 100.0 | 6 | 14 | US-10-015-328-5 |
| 8 | 26 | 100.0 | 6 | 14 | US-10-015-328-7 |
| 9 | 26 | 100.0 | 6 | 14 | US-10-015-328-11 |
| 10 | 26 | 100.0 | 9 | 14 | US-10-133-133A-10 |
| 11 | 26 | 100.0 | 9 | 14 | US-10-133-133A-20 |
| 12 | 26 | 100.0 | 6 | 14 | US-10-425-115-234557 |
| 13 | 26 | 100.0 | 71 | 15 | US-10-424-599-285243 |

| | | | | | | |
|----|----|-------|-----|----|----------------------|-------------------|
| 14 | 26 | 100.0 | 78 | 9 | US-09-795-501-10 | Sequence 10, Appl |
| 15 | 26 | 100.0 | 81 | 16 | US-10-437-963-135073 | Sequence 115073, |
| 16 | 26 | 100.0 | 91 | 16 | US-10-437-963-193303 | Sequence 193303, |
| 17 | 26 | 100.0 | 96 | 16 | US-10-437-963-173337 | Sequence 173337, |
| 18 | 26 | 100.0 | 109 | 17 | US-10-425-115-204973 | Sequence 204973, |
| 19 | 26 | 100.0 | 120 | 13 | US-10-036-444-4 | Sequence 4, Appl |
| 20 | 26 | 100.0 | 120 | 16 | US-10-767-701-41220 | Sequence 41220, A |
| 21 | 26 | 100.0 | 121 | 16 | US-10-767-701-40460 | Sequence 40460, A |
| 22 | 26 | 100.0 | 123 | 15 | US-10-425-115-229771 | Sequence 229771, |
| 23 | 26 | 100.0 | 124 | 15 | US-10-424-599-272233 | Sequence 272233, |
| 24 | 26 | 100.0 | 125 | 15 | US-10-392-837A-3 | Sequence 3, Appl |
| 25 | 26 | 100.0 | 126 | 14 | US-10-419-059-3 | Sequence 3, Appl |
| 26 | 26 | 100.0 | 126 | 14 | US-10-645-874-3 | Sequence 3, Appl |
| 27 | 26 | 100.0 | 129 | 15 | US-10-424-599-158168 | Sequence 158168, |
| 28 | 26 | 100.0 | 130 | 15 | US-10-392-837A-4 | Sequence 4, Appl |
| 29 | 26 | 100.0 | 130 | 15 | US-10-382-837A-5 | Sequence 5, Appl |
| 30 | 26 | 100.0 | 130 | 15 | US-10-392-837A-6 | Sequence 6, Appl |
| 31 | 26 | 100.0 | 135 | 15 | US-10-333-481-17 | Sequence 17, Appl |
| 32 | 26 | 100.0 | 145 | 16 | US-10-767-701-52098 | Sequence 52098, A |
| 33 | 26 | 100.0 | 151 | 14 | US-10-419-059-4 | Sequence 4, Appl |
| 34 | 26 | 100.0 | 151 | 16 | US-10-645-874-4 | Sequence 4, Appl |
| 35 | 26 | 100.0 | 153 | 14 | US-10-201-288-17 | Sequence 17, Appl |
| 36 | 26 | 100.0 | 161 | 16 | US-10-696-259-10 | Sequence 10, Appl |
| 37 | 26 | 100.0 | 162 | 15 | US-10-425-114-37635 | Sequence 37635, A |
| 38 | 26 | 100.0 | 163 | 17 | US-10-425-115-317745 | Sequence 317745, |
| 39 | 26 | 100.0 | 167 | 17 | US-10-425-115-344226 | Sequence 173977, |
| 40 | 26 | 100.0 | 170 | 16 | US-10-437-963-173977 | Sequence 48819, A |
| 41 | 26 | 100.0 | 171 | 15 | US-10-425-114-48819 | Sequence 8, Appl |
| 42 | 26 | 100.0 | 175 | 16 | US-10-696-259-8 | Sequence 5, Appl |
| 43 | 26 | 100.0 | 177 | 16 | US-10-696-259-5 | Sequence 7, Appl |
| 44 | 26 | 100.0 | 185 | 16 | US-10-696-259-7 | Sequence 2, Appl |
| 45 | 26 | 100.0 | 190 | 13 | US-10-036-444-2 | |

ALIGNMENTS

RESULT 1
US-09-728-653-8
Sequence 8, Application US/09728653
Publication NO. US20020123468A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
APPLICANT: Han, Amy Qi
TITLE OF INVENTION: Alpha-Ketamide Inhibitors of Hepatitis C Virus NS3 Protease
FILE REFERENCE: PR-7118
CURRENT APPLICATION NUMBER: US/09/728,653
CURRENT FILING DATE: 2000-12-01
PRIORITY APPLICATION NUMBER: US 60/166,998
PRIOR FILING DATE: 1999-12-03
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.
NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: N-terminal Protecting Group: t-Butoxycarbonyl
OTHER INFORMATION: Delta-Carboxy Ester: t-Butyl
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (2)..(2)
OTHER INFORMATION: Gamma-Carboxy Ester: t-Butyl
US-09-728-653-8
Query Match 100.0%; Score 26; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5
|
|
|
|
Db 1 DEVP 5

RESULT 2
US-10-015-328-8

; Sequence 8, Application US/10015328
; Publication No. US20030100768A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; APPLICANT: Han, Amy Qi
; APPLICANT: Glunz, Peter W.
; TITLE OF INVENTION: Imidazolidinones and Their Related Derivatives as Hepatitis C Virus
; FILE REFERENCE: PH-7203
; CURRENT APPLICATION NUMBER: US/10/015,328
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255,168
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: N-terminal Protecting Group: t-Butoxycarbonyl
; FEATURE:
; OTHER INFORMATION: Delta-Carboxy Ester: t-Butyl
; NAME/KEY: MOD RES
; LOCATION: (2)..(2)
; OTHER INFORMATION: Gamma-Carboxy Ester: t-Butyl
; US-10-015-328-8

Query Match 100.0%; Score 26; DB 14; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5
|
|
|
|
Db 1 DEVP 5

RESULT 3
US-09-728-653-5

; Sequence 5, Application US/09728653
; Publication No. US20020123468A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; APPLICANT: Han, Amy Qi
; APPLICANT: Glunz, Peter W.
; TITLE OF INVENTION: Alpha-Ketoamide Inhibitors of Hepatitis C Virus NS3 Protease
; FILE REFERENCE: PH-7118
; CURRENT APPLICATION NUMBER: US/09/728,653
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 60/168,998
; PRIOR FILING DATE: 1999-12-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.
; NAME/KEY: MISC_FEATURE

; LOCATION: (6)..(6)
; OTHER INFORMATION: Boro-allylglycine
; US-09-728-653-5

Query Match 100.0%; Score 26; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5
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|
|
|
Db 1 DEVP 5

RESULT 4
US-09-728-653-7

; Sequence 7, Application US/09728653
; Publication No. US20020123468A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; APPLICANT: Han, Amy Qi
; APPLICANT: Glunz, Peter W.
; TITLE OF INVENTION: Alpha-Ketoamide Inhibitors of Hepatitis C Virus NS3 Protease
; FILE REFERENCE: PH-7118
; CURRENT APPLICATION NUMBER: US/09/728,653
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 60/168,998
; PRIOR FILING DATE: 1999-12-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.
; NAME/KEY: MISC_FEATURE
; LOCATION: (6)..(6)
; OTHER INFORMATION: Boro-allylglycine pinanediol ester
; US-09-728-653-7

Query Match 100.0%; Score 26; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5
|
|
|
|
Db 1 DEVP 5

RESULT 5
US-09-728-653-11

; Sequence 11, Application US/09728653
; Publication No. US20020123468A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; APPLICANT: Han, Amy Qi
; APPLICANT: Glunz, Peter W.
; TITLE OF INVENTION: Alpha-Ketoamide Inhibitors of Hepatitis C Virus NS3 Protease
; FILE REFERENCE: PH-7118
; CURRENT APPLICATION NUMBER: US/09/728,653
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 60/168,998
; PRIOR FILING DATE: 1999-12-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.
; NAME/KEY: MISC_FEATURE

NAME/KEY: MOD RES
LOCATION: (1)..(1)
OTHER INFORMATION: N-terminal Protecting Group: t-Butoxycarbonyl
OTHER INFORMATION: Delta-Carboxy Ester: t-Butyl
FEATURE:
NAME/KEY: MOD RES
LOCATION: (2)..(2)
OTHER INFORMATION: Gamma-Carboxy Ester: t-Butyl
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (6)..(6)
OTHER INFORMATION: Boro-allylglycine pinanediol ester
US-09-728-653-11

Query Match 100.0%; Score 26; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVVP 5
Db 1 DEVVP 5

RESULT 6
US-10-010-184A-5
Sequence 5, Application US/10010184A
Publication No. US2003000828A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Pharma Company
APPLICANT: Priestly, et al.
TITLE OF INVENTION: No. US2003000828A1el Lactam Inhibitors of Hepatitis C Virus NS3
FILE REFERENCE: PH-7087-A
CURRENT APPLICATION NUMBER: US/10/010,184A
CURRENT FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: US 09/626,286
PRIOR FILING DATE: 2000-07-25
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: The synthesis of this peptide may be performed on an ABI 43A pepd
OTHER INFORMATION: ide synthesizer using readily available materials well known to c
OTHER INFORMATION: rdinarily skilled artisans
FEATURE:
NAME/KEY: misc feature
LOCATION: (6)..(6)
OTHER INFORMATION: 2-amino-4-penten-boronic acid
US-10-010-184A-5

Query Match 100.0%; Score 26; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVVP 5
Db 1 DEVVP 5

RESULT 7
US-10-015-328-5
Sequence 5, Application US/10015328
Publication No. US20030100768A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
APPLICANT: Han, Amy Qi
APPLICANT: Glunz, Peter W.
TITLE OF INVENTION: Imidazolidinones and Their Related Derivatives as Hepatitis C Vir
FILE REFERENCE: PH-7203
CURRENT APPLICATION NUMBER: US/10/015,328

CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 60/255,168
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.
NAME/KEY: MISC FEATURE
LOCATION: (6)..(6)
OTHER INFORMATION: Boro-allylglycine
US-10-015-328-5

Query Match 100.0%; Score 26; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVVP 5
Db 1 DEVVP 5

RESULT 8
US-10-015-328-7
Sequence 7, Application US/10015328
Publication No. US20030100768A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
APPLICANT: Han, Amy Qi
APPLICANT: Glunz, Peter W.
TITLE OF INVENTION: Imidazolidinones and Their Related Derivatives as Hepatitis C Vir
FILE REFERENCE: PH-7203
CURRENT APPLICATION NUMBER: US/10/015,328
CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 60/255,168
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.
NAME/KEY: MISC FEATURE
LOCATION: (6)..(6)
OTHER INFORMATION: Boro-allylglycine pinanediol ester
US-10-015-328-7

Query Match 100.0%; Score 26; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVVP 5
Db 1 DEVVP 5

RESULT 9
US-10-015-328-11
Sequence 11, Application US/10015328
Publication No. US20030100768A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
APPLICANT: Han, Amy Qi
APPLICANT: Glunz, Peter W.
TITLE OF INVENTION: Imidazolidinones and Their Related Derivatives as Hepatitis C Vir

TITLE OF INVENTION: Protease Inhibitors
FILE REFERENCE: PH-7203
CURRENT APPLICATION NUMBER: US/10/015,328
CURRENT FILING DATE: 2001-12-12
PRIORITY APPLICATION NUMBER: US 60/255,168
PRIORITY FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.
FEATURE:
NAME/KEY: MOD RES
LOCATION: (1)-(1)
OTHER INFORMATION: N-terminal Protecting Group: t-Butoxycarbonyl
OTHER INFORMATION: Delta-Carboxy Ester: t-Butyl
FEATURE:
NAME/KEY: MOD RES
LOCATION: (2)-(2)
OTHER INFORMATION: Gamma-Carboxy Ester: t-Butyl
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (6)-(6)
OTHER INFORMATION: Boro-allylglycine pinanediol ester
US-10-015-328-11

Query Match 100.0%; Score 26; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 1,4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVVP 5
|||||
DB 1 DEVVP 5

RESULT 10
US-10-133-133A-10
Sequence 10, Application US/10133133A
Publication No. US20030114385A1
GENERAL INFORMATION:
APPLICANT: CATHERS, Brian
APPLICANT: NEUTEBOON, Saskia
APPLICANT: SHEPARD, Michael
TITLE OF INVENTION: VIRAL ENZYME ACTIVATED PROTOXOPHORES
TITLE OF INVENTION: AND USE OF SAME TO TREAT VIRAL INFECTIONS
FILE REFERENCE: NB 2021.00
CURRENT APPLICATION NUMBER: US/10/133,133A
CURRENT FILING DATE: 2002-04-26
PRIORITY APPLICATION NUMBER: 60/286,983
PRIORITY FILING DATE: 2001-04-27
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Peptide sequence attached to prodrug compound
OTHER INFORMATION: activated by hepatitis C virus NS3 protease
FEATURE:
NAME/KEY: ACETYLATION
LOCATION: (1)...(0)
US-10-133-133A-10

Query Match 100.0%; Score 26; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1,4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVVP 5
|||||

Db 1 DEVVP 5
RESULT 11
US-10-133-133A-20
Sequence 20, Application US/10133133A
Publication No. US20030114385A1
GENERAL INFORMATION:
APPLICANT: CATHERS, Brian
APPLICANT: NEUTEBOON, Saskia
APPLICANT: SHEPARD, Michael
TITLE OF INVENTION: VIRAL ENZYME ACTIVATED PROTOXOPHORES
TITLE OF INVENTION: AND USE OF SAME TO TREAT VIRAL INFECTIONS
FILE REFERENCE: NB 2021.00
CURRENT APPLICATION NUMBER: US/10/133,133A
CURRENT FILING DATE: 2002-04-26
PRIORITY APPLICATION NUMBER: 60/286,983
PRIORITY FILING DATE: 2001-04-27
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 20
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Peptide sequence attached to prodrug compound
OTHER INFORMATION: activated by hepatitis C virus NS3 protease
FEATURE:
NAME/KEY: ACETYLATION
LOCATION: (1)...(0)
US-10-133-133A-20

Query Match 100.0%; Score 26; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1,4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVVP 5
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DB 1 DEVVP 5

RESULT 12
US-10-425-115-234557
Sequence 234557, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 234557
LENGTH: 67
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(67)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_145501C.1.pcp
US-10-425-115-234557

Query Match 100.0%; Score 26; DB 17; Length 67;
Best Local Similarity 100.0%; Pred. No. 1,5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVVP 5
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Db 33 DEVP 37

RESULT 13

US-10-424-599-285243
; Sequence 285243, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 285243
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_99603C.1.pep
US-10-424-599-285243

Query Match

Best Local Similarity 100.0%; Score 26; DB 15; Length 71;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5

Db 60 DEVP 64

RESULT 14

US-09-795-501-10
; Sequence 10, Application US/09795501
; Patent No. US20020042098A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel
; TITLE OF INVENTION: 32253 TRANSFERASE FAMILY MEMBERS AND
; FILE REFERENCE: 38155-20004.00
; CURRENT APPLICATION NUMBER: US/09/795,501
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/185,755
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Consensus amino acid sequence
US-09-795-501-10

Query Match

Best Local Similarity 100.0%; Score 26; DB 9; Length 78;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5

Db 4 DEVP 8

RESULT 15

US-10-437-963-135073
; Sequence 135073, Application US/10437963
; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 135073
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_36784C.1.pep
US-10-437-963-135073

Query Match

Best Local Similarity 100.0%; Score 26; DB 16; Length 81;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5

Db 43 DEVP 47

Search completed: December 8, 2004, 08:59:42
Job time : 143 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 8, 2004, 08:34:26 ; Search time 38 Seconds

(without alignments)
12.660 Million cell updates/sec

Title: SEQ1
Perfect score: 26
Sequence: 1 decomp 5

Scoring table:

BLASTSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

1: PIR 791:*
2: PIR1:*
3: PIR2:*
4: PIR3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | DB ID | Description |
|------------|-------|-------|--------|-------|-------------|
| 1 | 26 | 100.0 | 42 | 2 | G69113 |
| 2 | 26 | 100.0 | 74 | 2 | T19911 |
| 3 | 26 | 100.0 | 102 | 2 | T07890 |
| 4 | 26 | 100.0 | 108 | 2 | C89816 |
| 5 | 26 | 100.0 | 129 | 2 | F87109 |
| 6 | 26 | 100.0 | 150 | 2 | AC3294 |
| 7 | 26 | 100.0 | 151 | 1 | AMRU |
| 8 | 26 | 100.0 | 152 | 2 | AC3598 |
| 9 | 26 | 100.0 | 162 | 2 | T29728 |
| 10 | 26 | 100.0 | 170 | 2 | AD0114 |
| 11 | 26 | 100.0 | 176 | 2 | E95274 |
| 12 | 26 | 100.0 | 208 | 2 | G87475 |
| 13 | 26 | 100.0 | 214 | 2 | AB2195 |
| 14 | 26 | 100.0 | 225 | 2 | SS7810 |
| 15 | 26 | 100.0 | 249 | 2 | SS9404 |
| 16 | 26 | 100.0 | 287 | 2 | T32029 |
| 17 | 26 | 100.0 | 289 | 2 | S38770 |
| 18 | 26 | 100.0 | 289 | 2 | S17161 |
| 19 | 26 | 100.0 | 301 | 2 | C64448 |
| 20 | 26 | 100.0 | 327 | 2 | T42999 |
| 21 | 26 | 100.0 | 340 | 2 | T47371 |
| 22 | 26 | 100.0 | 344 | 2 | AG2882 |
| 23 | 26 | 100.0 | 346 | 2 | F97658 |
| 24 | 26 | 100.0 | 361 | 2 | AP3560 |
| 25 | 26 | 100.0 | 365 | 2 | T37720 |
| 26 | 26 | 100.0 | 366 | 2 | A11327 |
| 27 | 26 | 100.0 | 366 | 2 | AC1699 |
| 28 | 26 | 100.0 | 377 | 2 | T46149 |
| 29 | 26 | 100.0 | 393 | 2 | S72804 |

| | | | | | | |
|----|----|-------|-----|---|--------|-----------------------|
| 30 | 26 | 100.0 | 393 | 2 | S23409 | FUN20 protein - ye |
| 31 | 26 | 100.0 | 395 | 2 | S75952 | hypothetical prote |
| 32 | 26 | 100.0 | 399 | 2 | G75332 | acetyl-CoA acetyl |
| 33 | 26 | 100.0 | 411 | 2 | S26195 | probable carboxyl- |
| 34 | 26 | 100.0 | 418 | 2 | T39230 | hypothetical prote |
| 35 | 26 | 100.0 | 419 | 2 | AG0046 | probable membrane |
| 36 | 26 | 100.0 | 424 | 1 | XNBYP | choline-phosphate |
| 37 | 26 | 100.0 | 432 | 2 | T30597 | enoyl-CoA hydratase |
| 38 | 26 | 100.0 | 433 | 2 | T48118 | hypothetical prote |
| 39 | 26 | 100.0 | 436 | 2 | T00756 | hypothetical prote |
| 40 | 26 | 100.0 | 449 | 2 | D69476 | TBP-interacting pr |
| 41 | 26 | 100.0 | 450 | 2 | E98303 | hypothetical 49.3K |
| 42 | 26 | 100.0 | 450 | 2 | AH2979 | ultraviolet-sensitive |
| 43 | 26 | 100.0 | 455 | 2 | S05573 | deoxyribodipyrimid |
| 44 | 26 | 100.0 | 460 | 2 | T47108 | serine-tRNA ligase |
| 45 | 26 | 100.0 | 467 | 2 | E69601 | ATP-dependent Clp |

ALIGNMENTS

RESULT 1
G69113
hypothetical protein MTH1845 - Methanobacterium thermoautotrophicum (strain Delta H)
C/Species: Methanobacterium thermoautotrophicum
C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C/Accession: G69113
R/Smith, D.R.; Doucette-Stamm, L.A.; Delonghery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Ki, S.; Church, G.M.; Viscare, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Javan, N.
J. Bacteriol. 179, 7135-7155, 1997
A/Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func
A/Reference number: A69000; MIMD:98037514; PMID:9371463
A/Accession: G69113
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-42 <MTH>
A/Cross-references: UNIPROT:Q27873; GB:AE000937; GB:AE000666; NID:G2622974; PIDN:AB86311
A/Experimental source: strain Delta H
C/Genetics:
A/Gene: MTH1845

Query Match
Best Local Similarity 100.0%; Score 26; DB 2; Length 42;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVVP 5
Db 35 DEVVP 39

RESULT 2
T19911
hypothetical protein C43F9.7 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
R/Morimore, B.
submitted to the EMBL Data Library, November 1996
A/Reference number: Z19195
A/Accession: T19911
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-74 <MTH>
A/Cross-references: UNIPROT:Q9XUG8; EMBL:Z82262; PIDN:CA05150.1; GSPDB:GN00022; CESP:CA
A/Experimental source: clone C43F9
C/Genetics:
A/Gene: CESP:C43F9.7
A/Map position: 4
A/Introns: 23/1; 47/2

Query Match
Best Local Similarity 100.0%; Score 26; DB 2; Length 74;
Matches 100.0%; Pred. No. 25;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DEVP 5
 |||||
 Db 30 DEVP 34

RESULT 3

T07890
 protein kinase (BC 2.7.1.-) 5 - tomato (fragment)
 C:Species: Lycopersicon esculentum (tomato)
 C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 16-Aug-2004
 C:Accession: T07890
 R:Zhang, S.; Diener, T.O.
 submitted to the EMBL Data Library, February 1997
 A:Description: Isolation and characterization of seven serine/threonine protein kinase-c
 A:Reference number: 216191
 A:Accession: T07890
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-102 <ZHA>
 A:Cross-references: UNIPROT:Q49991; EMBL:U89682; NID:g2735253; PIDN:AAB93863.1; PID:g273
 A:Experimental source: cultivar Rutgers; seedling
 C:Genetics:
 A:Gene: PK5
 C:Superfamily: protein kinase homology
 C:Keywords: phosphotransferase

Query Match 100.0%; Score 26; DB 2; Length 102;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5
 |||||
 Db 27 DEVP 31

RESULT 4

C89816
 hypothetical protein spovg [imported] - Staphylococcus aureus (strain N315)
 C:Species: Staphylococcus aureus
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
 C:Accession: C89816
 R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
 ma, A.; Mizutani-U, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 Lancet 357, 1225-1240, 2001
 A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
 A:Reference number: A89758; MUID:21311952; PMID:11418146
 A:Accession: C89816
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-108 <KUR>
 A:Cross-references: UNIPROT:Q99WA5; GB:BA000018; PID:g13700388; PIDN:BA841686.1; GSPDB:G
 A:Experimental source: strain N315
 C:Genetics:
 A:Gene: spovg
 C:Superfamily: stage V sporulation protein spovg

Query Match 100.0%; Score 26; DB 2; Length 108;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5
 |||||
 Db 92 DEVP 96

RESULT 5

F87109
 hypothetical protein [imported] - Mycobacterium leprae
 C:Species: Mycobacterium leprae
 C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004

C:Accession: F87109
 R:Cole, S.T.; Eiglmeyer, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hor
 R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Fellwell, T.; Fraser, A.; Hamlin, N.; Holtroyd,
 R.; M.A.; Rutherford, K.M.
 Nature 409, 1007-1011, 2001
 A:Authors: Rutherford, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
 A:Title: Massive gene decay in the leprosy bacillus.
 A:Reference number: A86909; MUID:21128732; PMID:11234002
 A:Accession: F87109
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-129 <STO>
 A:Cross-references: UNIPROT:Q9CBT7; GB:AL450380; NID:g13093395; PIDN:CMC30555.1; GSPDB:G
 C:Genetics:
 A:Gene: ML1604

Query Match 100.0%; Score 26; DB 2; Length 129;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5
 |||||
 Db 22 DEVP 26

RESULT 6

AC3294
 biopolymer transport exbd protein [imported] - Brucella melitensis (strain 16M)
 C:Species: Brucella melitensis
 C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
 C:Accession: AC3294
 R:DeVecchio, V.G.; Kapatal, V.; Redkar, R.J.; Parra, G.; Mujer, C.; Los, T.; Ivanova, I
 Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Levesc
 Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
 A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
 A:Reference number: AD3252; PMID:11756688
 A:Accession: AC3294
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-150 <KUR>
 A:Cross-references: UNIPROT:O8YIV3; GB:AE008917; PIDN:AAL51518.1; PID:g17982233; GSPDB:G
 A:Experimental source: strain 16M
 C:Genetics:
 A:Gene: BMEI0337
 A:Map position: 1
 C:Superfamily: tolR protein

Query Match 100.0%; Score 26; DB 2; Length 150;
 Best Local Similarity 100.0%; Pred. No. 55;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5
 |||||
 Db 94 DEVP 98

RESULT 7

AMH1
 natriuretic peptide A precursor [validated] - human
 N:Alternate names: ANP; atrial natriuretic factor; atrial natriuretic protein; prepronat
 N:Contains: atrial alpha natriuretic peptide (ANP); cardiodilatin (atrial gamma natriuret
 C:Species: Homo sapiens (man)
 C:Date: 15-Nov-1984 #sequence_revision 15-Nov-1984 #text_change 09-Jul-2004
 C:Accession: A22693; B22693; A01424; B29370; A23733; I58054; S14097; I39458; I39459; I39
 R;Nemer, M.; Chamberland, M.; Sirois, D.; Argentin, S.; Drouin, J.; Dixon, R.A.F.; Zivin
 Nature 312, 654-656, 1984
 A:Title: Gene structure of human cardiac hormone precursor, pronatriodilatin.
 A:Reference number: A22693; MUID:85061626; PMID:6095118
 A:Accession: A22693
 A:Molecule type: DNA
 A:Residues: 1-151 <NEM>
 A:Cross-references: UNIPROT:P01160; GB:X01470; NID:g28687; PIDN:CAA25699.1; PID:g825625
 A:Accession: B22693

A:Molecule type: DNA
 A:Residues: 1-151, 'RR' <NE2>
 A>Note: allelic variant with UGA termination codon replaced by CGA arginine codon
 R:Okawa, S.; Imai, M.; Ueno, A.; Tanaka, S.; Noguchi, T.; Nakazato, H.; Kangawa, K.; Furutani, Y.; Matsuo, H. Nature 309, 724-726, 1984
 A>Title: Cloning and sequence analysis of cDNA encoding a precursor for human atrial natriuretic factor
 A:Reference number: A01424; MUID:84129199; PMID:6203042
 A:Accession: A01424
 A:Molecule type: mRNA
 A:Residues: 1-151 <OK>
 A:Cross-references: GB:K02043; NID:9178629; PIDN:AA59379.1; PID:9178630
 R:Seidman, C.E.; Bloch, K.D.; Klein, K.A.; Smith, J.A.; Seidman, J.G. Science 226, 1206-1209, 1984
 A>Title: Nucleotide sequences of the human and mouse atrial natriuretic factor genes.
 A:Reference number: A29370; MUID:85065766; PMID:6542248
 A:Accession: B29370
 A:Molecule type: DNA
 A:Residues: 1-64, 'D', '66-151' <SE1>
 A:Cross-references: GB:K02043
 R:Kangawa, K.; Matsuo, H. Biochem. Biophys. Res. Commun. 118, 131-139, 1984
 A>Title: Purification and complete amino acid sequence of alpha-human atrial natriuretic factor
 A:Reference number: A32733; MUID:84128019; PMID:6230082
 A:Accession: A32733
 A:Molecule type: protein
 A:Residues: 124-151 <KAN>
 R:Nakayama, K.; Ohkubo, H.; Hirose, T.; Inayama, S.; Nakanishi, S. Nature 310, 699-701, 1984
 A>Title: mRNA sequence for human cardiocalin-atrial natriuretic factor precursor and A:Reference number: 158054; MUID:84295577; PMID:6547996
 A:Accession: 158054
 A:Molecule type: mRNA
 A:Residues: 1-151 <RES>
 A:Cross-references: GB:M30262; NID:9180181; PIDN:AAA35669.1; PID:9180182
 R:Vanheste, Y.; Michel, A.; Deschodt-Lanckman, M. Eur. J. Biochem. 196, 281-286, 1991
 A>Title: Hydrolysis of intact and Cys-Phe-cleaved human atrial natriuretic peptide in vitro
 A:Reference number: S14097; MUID:91176996; PMID:1826098
 A:Accession: S14097
 A:Molecule type: protein
 A:Residues: 124-151 <VAN>
 A>Note: natural and synthetic peptide subjected to kallikrein proteolysis
 R:Zivin, R.A.; Condeelis, J.H.; Dixon, R.A.; Seidman, M.G.; Chretien, M.; Nemer, M.; Chamberlain, D. Natl. Acad. Sci. U.S.A. 81, 6325-6329, 1984
 A>Title: Molecular cloning and characterization of DNA sequences encoding rat and human atrial natriuretic factor
 A:Reference number: I39458; MUID:85038509; PMID:6238331
 A:Accession: I39458
 A:Molecule type: preliminary; translated from GB/EMBL/DBJ
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 119-151, 'RR' <RE2>
 A:Cross-references: GB:K02044; NID:9178631; PIDN:AAA51730.1; PID:9178632
 R:Maki, M.; Parmentier, M.; Inagami, T. Biochem. Biophys. Res. Commun. 125, 797-802, 1984
 A>Title: Cloning of genomic DNA for human atrial natriuretic factor.
 A:Reference number: I39459; MUID:850696983; PMID:6097248
 A:Accession: I39459
 A:Molecule type: preliminary; translated from GB/EMBL/DBJ
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-75 <RE3>
 A:Cross-references: GB:K02399; NID:9178633; PIDN:AAA5528.1; PID:9178634
 R:Seidman, C.E.; Bloch, K.D.; Zisfein, J.; Smith, J.; Haber, E.; Homcy, C.J.; Duby, A.D.; Hyperkalemia, J. 31-34, 1985
 A>Title: Molecular studies of the atrial natriuretic factor gene.
 A:Reference number: I39460
 A:Accession: I39460
 A:Molecule type: preliminary; translated from GB/EMBL/DBJ
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-64, 'D', '66-151' <RE4>
 A:Cross-references: GB:M54951; NID:9178636; PIDN:AAA35529.1; PID:9178638
 R:Greenberg, B.D.; Bensen, G.H.; Sellhammer, J.J.; Lewicki, J.A.; Fiddes, J.C. Nature 312, 656-658, 1984
 A>Title: Nucleotide sequence of the gene encoding human atrial natriuretic factor precursor

A:Reference number: I37167; MUID:85061627; PMID:6095119
 A:Accession: I37167
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 26-151 <RE5>
 A:Cross-references: EMBL:X01471; NID:928690; PIDN:CAA25700.1; PID:91340150
 C:Comment: Cardiolipin is a vasodilator but not a diuretic or natriuretic.
 C:Genetics:
 A:Gene: GDB:NPPA; ANP; PND
 A:Cross-references: GDB:I18727; OMIM:108780
 A:Map position: 1p36-1p36
 A:Insertions: 41/3; 150/3
 C:Superfamily: natriuretic peptide A precursor
 C:Keywords: atrium; diuretic; hormone; natriuretic; osmoregulation
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:126-151/Product: cardiolipin #status predicted <SIG>
 F:124-151/Product: atrial alpha natriuretic peptide #status experimental <ANP>
 F:130-146/Dissulfide bonds: #status experimental

Query Match 100.0%; Score 26; DB 1; Length 151;
 Best Local Similarity 100.0%; Pred. No. 55;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Ox 1 DEVP 5
 Db 55 DEVP 59

RESULT 8
 AC3598
 ebsc protein [imported] - Brucella melitensis (strain 16M)
 C:Species: Brucella melitensis
 C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
 C:Accession: AC3598

R:Delvecchio, V.G.; Kapatal, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, P.; Mazur, M.; Goldstein, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Leless, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
 A>Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
 A:Reference number: AD3552; PMID:11756688
 A:Accession: AC3598
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-152 <KIR>
 A:Cross-references: UNIPROT:Q8YCS5; GB:AE008918; PIDN:AAU53950.1; PID:917984896; GSPDB:C.C
 A:Experimental source: strain 16M
 C:Genetics:
 A:Gene: BMEI10708
 A:Map position: II

Query Match 100.0%; Score 26; DB 2; Length 152;
 Best Local Similarity 100.0%; Pred. No. 56;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Ox 1 DEVP 5
 Db 119 DEVP 123

RESULT 9
 T29728
 hypothetical protein K0394.7 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 R:Du, Z.; Le, T.T.; Kemp, K.
 submitted to the EMBL Data Library, April 1996
 A:Description: The sequence of C. elegans cosmid K0394.
 A:Reference number: Z20673
 A:Accession: T29728
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-162 <DUT>
 A:Cross-references: UNIPROT:Q21175; EMBL:U55370; PIDN:AAA97999.1; GSPDB:GN00023; CESP:KO:

A:Experimental source: strain Bristol N2; clone K03B4
 C:Genetics:
 A:Gene: CESP:K03B4.7
 A:Map position: 5
 A:introns: 58/3; 105/3

Query Match 100.0%; Score 26; DB 2; Length 162;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5
 DB 22 DEVP 26

RESULT 10

AD0114 conserved hypothetical protein YPO0932 [imported] - Yersinia pestis (strain CO92)

C:Species: Yersinia pestis
 C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
 C:Accession: AD0114
 R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Hill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett, Nature 413, 523-527, 2001
 A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A:Reference number: AB0001; MUID:21470413; PMID:11586360
 A:Accession: AD0114

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-170 <KUR>
 A:Cross-references: UNIPROT:Q8ZH6; GB:AL590842; PIDD:GNC89775.1; PID:g15979002; GSPDB:G
 C:Genetics:
 A:Gene: YPO0932
 C:Superfamily: hypothetical protein H1173

Query Match 100.0%; Score 26; DB 2; Length 170;
 Best Local Similarity 100.0%; Pred. No. 63;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5
 DB 73 DEVP 77

RESULT 11

B55274 hypothetical protein SMA0191 [imported] - Sinorhizobium meliloti (strain 1021) megaplasm
 C:Species: Sinorhizobium meliloti
 C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004

C:Accession: E95274
 R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows
 Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
 A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti
 A:Reference number: A95262; MUID:21396509; PMID:11481432

A:Accession: E95274
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-176 <KUR>

A:Cross-references: UNIPROT:Q930U3; GB:AE006469; PIDD:AAK64759.1; PID:g14523165; GSPDB:G
 A:Experimental source: strain 1021, megaplasmid pSymA
 R:Galbert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
 P.; Chain, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
 L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001
 A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
 hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.

A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
 A:Reference number: A96039; MUID:2136234; PMID:11474104

A:Contents: annotation
 C:Genetics:
 A:Gene: SMA0191

A:Genome: plasmid

Query Match 100.0%; Score 26; DB 2; Length 176;
 Best Local Similarity 100.0%; Pred. No. 66;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5
 DB 62 DEVP 66

RESULT 12

G87475 conserved hypothetical protein CCI828 [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus
 C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
 C:Accession: G87475
 R:Neuman, W.C.; Feldlyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.I.
 B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolont
 n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A:Title: Complete Genome Sequence of Caulobacter crescentus.
 A:Reference number: A87249; MUID:21173698; PMID:11259647

A:Accession: G87475
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-208 <STD>
 A:Cross-references: UNIPROT:Q9A798; GB:AE005673; NID:g13423265; PIDD:AAK23803.1; GSPDB:G
 C:Genetics:
 A:Gene: CCI828

Query Match 100.0%; Score 26; DB 2; Length 208;
 Best Local Similarity 100.0%; Pred. No. 79;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5
 DB 14 DEVP 18

RESULT 13

AB2195 serine esterase [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp. PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C:Accession: AB2195
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kunitz, T.; Sasamoto, S.; Watanabe, A.; Iriyuchi
 Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
 DNA Res. 8, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
 A:Reference number: AB1807; MUID:21595285; PMID:1175840

A:Accession: AB2195
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-214 <KUR>
 A:Cross-references: UNIPROT:Q8YSH2; GB:BA000019; PIDD:BAE74812.1; PID:g17132207; GSPDB:G
 A:Experimental source: strain PCC 7120
 C:Genetics:

A:Gene: al13113

Query Match 100.0%; Score 26; DB 2; Length 214;
 Best Local Similarity 100.0%; Pred. No. 82;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5
 DB 164 DEVP 168

RESULT 14

S57810 hypothetical protein precursor (clone TPP11) - tomato

C/Species: Lycopersicon esculentum (tomato)
 C/Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
 C/Accession: S57810
 R/Milligan, S.B.; Gaesser, C.S.
 Plant Mol. Biol. 28, 691-711, 1995
 A/Title: Nature and regulation of p1stf1-expressed genes in tomato.
 A/Reference number: S57808; MUID:95375233; PMID:7647301
 A/Accession: S57810
 A/Status: preliminary; nucleic acid sequence not shown
 A/Molecule type: mRNA
 A/Residues: 1-225 <MIL>
 A/Cross-references: UNIPROT:Q04129; EMBL:U20592; NID:9624625; PIDN:AAA80497.1; PID:99246
 C/Superfamily: plant Kunitz-type proteinase inhibitor

Query Match 100.0%; Score 26; DB 2; Length 225;
 Best Local Similarity 100.0%; Pred. No. 87;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVVP 5
 |||||
 Db 32 DEVVP 36

RESULT 15

S59404
 hypothetical protein YLR435w - yeast (Saccharomyces cerevisiae)
 N/Alternate names: hypothetical protein L9753.3
 C/Species: Saccharomyces cerevisiae
 C/Date: 30-Nov-1995 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
 C/Accession: S59404
 R/Du, Z.
 submitted to the EMBL Data Library, February 1995
 A/Description: The sequence of S. cerevisiae cosmid 9753.
 A/Reference number: S59401
 A/Accession: S59404
 A/Molecule type: DNA
 A/Residues: 1-249 <DUZ>
 A/Cross-references: UNIPROT:Q06672; EMBL:U21094; NID:9665967; PIDN:AAB67515.1; PID:96659
 A/Experimental source: strain S288C (AB972)
 C/Genetics:
 A/Gene: MIPS:YLR435w
 A/Cross-references: SGD:S0004427
 A/Map position: 12R

Query Match 100.0%; Score 26; DB 2; Length 249;
 Best Local Similarity 100.0%; Pred. No. 97;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVVP 5
 |||||
 Db 218 DEVVP 222

Search completed: December 8, 2004, 08:56:31
 Job time : 41 secs

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